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Post-processing: Minimum Match 0%
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SOURCE ORGA REFERE AUTH	RESULT 108277 LOCUS DEFINIO ACCESS VERSION																												20	200	700/6		Result No.	
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59) glyceraldehyde-3-phosphate	459 bp nt EP 0374913.	ALIGNMENTS	பா	CJU76923	HUMLSZA	GGU76913	BC004147 SSU76921	E02193	E01888	HUMLSZH	PTU76912	CELYS	рн076919	MMLYS	BOVLYSOZYM	PELYSOC	TFU76918	TOU76917	BOVLSZ2DA	BOYLZYM14D	AXILZM1	SHPLZM4B	SHPLZMlA	SHPLZMIC SHPLZM2A	SHPLZM1B	SHPLZM3A	BOVLSZ1A	BOVLSZ1B	109315	BOVLSZ2A	BOVLZYM7A	I08277 BOVLSZ2B	ID	
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Irwin, D.M. and Wilson, A.C.
                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Cet
Bovidae; Bovinae; Bos
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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lysozyme.
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                  /protein_id="AAA30629.1"
/db_xref="GI:163317"
                                               /codon_start
                                                       /note="lysozyme 2b precursor"
                                                                                    /organism="Bos taurus"
/db_xref="taxon:9913"
translation="MKALVILGFLFLSVAVQGKVFERCELARTLKKLGLDGYKGVSLA"
                                                                                                                             ocation/Qualifiers
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                                                                                                                            Multiple cDNA sequences of bovine tracheal lysozyme J. Biol. Chem. 268 (36), 27440-27446 (1993) 94086565
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Stewart,C.B. and Basbaum,C.
                                                                                                                                                                                              Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovinae; Bos.
1 (bases 1 to 1060)
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  D
           /organism="Bos taurus"
/db_xref="taxon:9913"
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/tissue_type="trachea"
/dev_stage="adult"
                                                                                               Location/Qualifiers
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MENDIAKAVACAKHIVSEQGITAWVAWKSHCRDHDVSSYVEGCTL"
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162 c 194 g
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Sequence 1 from patent US 5422108,
112256
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                                                                                                                                                                                                                                                                                              Mirkov,T.Erik. and Fitzmaurice,L.C.
Protection of plants against plant pathogens
Patent: US 5422108-A 1 06-JUN-1995;
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                                            GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTTGGACTGGACGGCTATAAGGGAGTCAG
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Pred. No. 3.5e-110;
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Irwin, D.M. and Wilson, A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                Draft entry and computer-readable sequence by D.M.Irwin, 23-JUN-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89291894
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                                            GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG
                                                                         GGCTCTCGTTATTCTGGGGTTTCTCTTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGA 65
Biol. Chem. 264 (19), 11387-11393 (1989)
                                                                                                                                                                               282
                                                                                                       Conservative
                                                                                                                                                                                                         /note="lysozyme 2a signal peptide" 50. 436
                                                                                                                                                                            /product="lysozyme
154 c 187 g
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/protein_id="AAA30628.1"
/protein_id="AAA30628.1"
/db_xref="GI:163315"
/translation="TLVILGFLFLSVAVQGKVFERCELARTLKKLGLDGYKGVSLANW
/translation="TLVILGFLFLSVAVQGKVFERCELARTLKKLGLDGYKGVSLANW
LCLTKWESSYNTKATNYNPSSESTDYGIFQINSKWWCNDGKTPNAVDGCHVSCSELME
NDIAKAVACAKHIVSEQGITAWVAWKSHCRDHDVSSYVEGCTL"
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/db_xref="taxon:9913"
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Pred. No. 9.7e-110;
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                                                                                                                                                                                                                                              σ
                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 963)
Digan, M.E., Harpold, M.M., Lair, S.V., Thill, G.P., Siegel, R.S., Ellis, S.B. and Williams, M.E.
PRODUCTION OF ANIMAL LYSOZYME c VIA SECRETION FROM PICHIA PASTORIS AND COMPOSITION THEREFOR PATENT: WO 8904320-A 1 18-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1 from Patent WO 109315 109315.1 GI:587976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109315
                                                                                                                                                                                                                                                                                    Similarity
  CCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAA 185
                                                                                                                                                            GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG
                                                                                                         GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG
                                                                                                                                                                                                                               GGCTCTCGTTATTCTGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGA
                            GTGTAATGATGCCAAAACCCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATT
                                                                                                                                                                                                                  GACTCTCGTTATTCTGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGA
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                                                                                                                                                                                                                                                                                 Score 437.4; DB 6; Pred. No. 9.6e-110;
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O 8904320.
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TITLE
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Best Local Similarity
                                                                                                                                                                                                                                                                                 COUNT
                                                                                                                                                                                                                                                                                                        mat_peptide
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89291894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1082 bp
BOVLS23A 1082 bp
Bovine lysozyme c isozyme 3a mRNA,
M26242 J04831 M27180
M26242.1 GI:163322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Draft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Multiple cDNA sequences and the evolution of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 1082)
Irwin, D.M. and Wilson, A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine abomasum, cDNA to mRNA, clone lambda-cBL[26,28].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lysozyme
             ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 240
                                                                GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT 180
                                                                                                                    TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120
                                                                                                                                                                       ATGAAGGCTCTCGTTATTCTGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTC
                                                                                                     TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGATGGCTATAAGGGA 128
ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                  GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT 188
                                                                                                                                                           ATGAAGGCTCTCATTATTCTGGGGTTTCTCTTCTTTCTGTCGCTGTCCAAGGCAAGGTC
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                                                                                                                                                                                                                                                                                 343
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry and computer-readable sequence M.Irwin, 23-JUN-1989.
                                                                                                                                                                                                                                                                                                       /note="lysozyme 3a signal peptide"
63. .449
                                                                                                                                                                                                                                                                                                                                          /translation="MKALIILGFLELSYAVQGKVFERCELARTLKKLGLDGYKGYSLANULCLTKWESSYNTKATNYNPSSESTDYGIFQINSKWWCNDGKTPNAVDGCHVSCSELMENDIAKAVACAKHIVSEQGITAWVAWKSHCRDHDVSSYVQGCTL"
                                                                                                                                                                                                                                                                             /product="lysozyme 3a"
205 c 209 a
                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAA30632.1"
/db_xref="GI:163323"
                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                         /note="lysozyme 3a precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                          96.0%;
97.5%;
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                                                                                                                                                                                                                           Score 426.4; DB Pred. No. 1e-106;
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Best Local S
Matches 429
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128
                        121
                                                                   61 TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120
                                                   68 TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGATGGCTATAAGGGA
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Bovine lysozyme c isozyme 1b mRNA, complete cds.
M26246 J04831 M27179
M26246.1 GI:163312
                                                                                                        8
                                                                                                                     1 ATGAAGGCTCTCGTTATTCTGGGGTTTCCTTTCCTTTCTGTCGCTGTCCAAGGCAAGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Draft entry and computer-readable by D.M.Irwin, 23-JUN-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multiple cDNA sequences and the evolution of bovine stomach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 891)
Irwin,D.M. and Wilson,A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovine abomasum, cDNA to mRNA, clones lambda-cBL[3,4,35].
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GTCAGTCTGGCAAACTGGCTGTTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT 187
                                                                                                        ATGAAGGCTCTCATTATTCTGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 264 (19), 11387-11393 (1989)
                                                                                                                                                                                                                                 274
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                           /note="lysozyme 1b signal peptide"
62. .448
                                                                                                                                                                                                                               /product="lysozyme lb"
152 c 196 g
                                                                                                                                                                                                                                                                                                 NWLCLTKWESSYNTKATNYNPGSESTDYGIFQINSKWWCNDGKTPNAVDGCHVSCSEL
MENEIAKAVACAKQIVSEQGITAWVAWKSHCRDHDVSSYVEGCTL"
                                                                                                                                                                                                                                                                                                                                        /protein_id="AAA30627.1"
/db_xref="GI:163313"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  /note="lysozyme 1b precursor"
                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                            translation-"MKALIILGFLFLSVAVQGKVFERCELARTLKKLGLDGYKGVSLA
                                                                                                                                                                                                                                                                                                                                                                     codon_start=
                                                                                                                                                                          94.6%;
                                                                                                                                                            Score 420; DB 4;
Pred. No. 6e-105;
0; Mismatches 1
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                                                                                                                                                                                       DB 4; Length 891;
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AUTHORS
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ACCESSION
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PUBMED
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                                                                                                                                                                                                                               sig_peptide
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                                                                                                             427;
                                                      23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovine lysozyme c isozyme la mRNA,
M26245 J04831 M27178
M26245.1 GI:163310
                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. 264 (19), 11387-11393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovidae; Bovinae; Bos.
1 (bases 1 to 906)
Irwin,D.M. and Wilson,A.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                           2738070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine abomasum, cDNA to mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lysozyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BOVLSZ1A
                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATGTTGAGGGTTGCACGCTGTAA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACGTTGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                             276
                                                                                                           Conservative
                                                                                                                                                                                                        /note="lysozyme la signal peptide"
77. .463
                                                                                                                                                                            /product="lysozyme la"
155 c 198 g
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  /codon_start=
                                                                                                                                                                                                                                                                                                                            /note="lysozyme la precursor"
                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                        /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                      .906
                                                                                                                       93.9%;
96.2%;
                                                                                                           0
                                                                                                          Score 416.8; DB 4;
Pred. No. 4.6e-104;
0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            906 bp
                                                                                                                                                                                277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
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Draft entry and computer-readable sequence for by D.M.Irwin, 23-JUN-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multiple cDNA sequences and the evolution of bovine stomach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGTGGTGTAATGATGGCAAAACCCCCCAACGCAGTTGACGGCTGTCATGTATCCTGCAGC
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                                                                                                     /protein_id="aaa30626.1"
/protein_id="aaa30626.1"
/db_xref="01:163311"
/translation="mkalilideflelsyavogkveercelartlkkldldgykgvsla
/translation="mkalilideflelsyavogkveercelartlkkldldgykgvsla
verdeltkwessyntkalnynpgsesstdygifqinskwwcndgktpnavdgchvscsel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MENEIAKAVACAKQIVSEQGITAWVAWKSHCRDHDVSSYVEGCTL'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone lambda-cBL21.
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                                                                                                                                                                                                                                                            Length 906;
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ORIGIN
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                                                                     Query Match
Best Local (
                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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                                                                                                                                                 mat_peptide
                                                                                                                                                                             sig_peptide
                                                                                                                                                                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          443 TATGTTGAGGGTTGCACGCTGTAA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421
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                               46
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                                                                                                                                                                                                                                                                                                                                                  Draft entry and computer-readable sequence for [1] kindly submitted by D.M.Irwin, 23-JUN-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovidae; Bovinae; Bos.
1 (bases 1 to 877)
Irwin,D.M. and Wilson,A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovine lysozyme c isozyme M26244 J04831 M27183
                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                2738070
                                                                                                                                                                                                                                                                                                                                                                                                                             Multiple cDNA sequences and the evolution of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovine abomasum, cDNA to mRNA, clones lambda-cBL[20,36,39].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M26244.1 GI:163318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BOVLS22C
                                                                                                                                                                                                                                                                                                                                                                                                                     Lysozyme
 GTCAAAGGCAAGGTCTTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTG
                GTCCAAGGCAAGGTCTTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAAACTACAATCCTGGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGTGGTGTAATGATGGCAAAACCCCCCAACGCAGTTGACGGCTGTCATGTATCCTGCAGC
                                                                                                                          285
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    Chem. 264 (19), 11387-11393 (1989)
                                                                                                                                                 /note="lysozyme 2c signal peptide"
10. .396
                                                                                                                                                                                    /protein_id="AAA30630.1"
/db_xref="G1:163319"
/db_xref="G1:163319"
/translation="VKGKVFERCELARTLKKLGLDGYKGVSLANWLCLTKWESSYNTK
/translation="VKGKVFERCELARTLKKLGLDGYKGVSLANWLCLTKWESSYNTK
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VSEQGITAWVAWKSHCRDHDVSSYVEGCTL"
                                                                                                                       /product="lysozyme
142 c 181 g
                                                                                                                                                                                                                                                                                    /db_xref="taxon:9913"
<1. .399
                                                                                                                                                                                                                                                         /codon_start=
                                                                                                                                                                                                                                                                  /note="lysozyme 2c precursor"
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                           organism="Bos taurus"
                                                                     89.5%;
99.7%;
                                                       0,
                                                      Score 397.4; DB 4;
Pred. No. 1e-98;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            877
2c
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                                                    0;
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AUTHORS
TITLE
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                      Qy
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
MEDLINE
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                                                               Query Match
Best Local
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ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sheep abomasum, cDNA to mRNA. Ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHPLZM3A 875 bp
Sheep lysozyme 3a (lyz3a) mRNA,
M32496 J05279
M32496.1 GI:165971
                                                                                                                                                                                                                                                                                                                                             Draft entry and computer-readable by D.M.Irwin, 01-MAR-1990.
                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                          2318875
                                                                                                                                                                                                                                                                                                                                                                                                                                       Irwin, D.M. and Wilson, A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lysozyme 3a.
                                                                                                                    278
                                                   Conservative
                                                                                                                   Ø
                                                                                                                                             /product="lysozyme 3a"
1. .17
                                                                                                                /note="PCR primer"
148 c 189 g
                                                                                                                                                                                 QGITAWVAWKSHCRDHDVSSYVEGCTL"
                                                                                                                                                                                                                                                               /note="lysozyme 3a precursor"
                                                                                                                                                                                                                                                                              <1. .390
                                                                                                                                                                                                                                                                                       /organism="Ovis aries"
/db_xref="taxon:9940"
                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                   /codon_start
                                                              82.8%;
96.4%;
                                                   0;
                                                   Mismatches
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406 CATGACGTCAGCAGTTACGTTGAGGGTTGCACCCTGTAA 444
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                                        55 AAGGTCTTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 CATATTGTCAGTGAGCAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Caprinae; Ovis.
1 (bases 1 to 875)
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CATGTATCCTGCAGCGAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAG
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                                                                                                                                                                                                                                                                                                       /protein_id="AAA31561.1"
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/tzans1ation="KyFERCELARTLKKLGLDGYKGVSLANWLCLTKWESGYNTKATN
YNPGSESTDYGIFQINSKWWCNDGKTPNAVDGCHVSCSALMENDIEKAVACAKHIVSE
                                                                                                  Score 367.6; DB 4
Pred. No. 1.6e-90;
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Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 881)
1 (bases 1 to 881)
1 rwin,D.M. and Wilson,A.C.
Concerted evolution of ruminant stomach lysozymes. Characterizatic
of lysozyme cDNA clones from sheep and deer
J. Biol. Chem. 265 (9), 4944-4952 (1990)
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by D.N
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                AAGGTCTTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTAT
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 AAGGTCTTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGGAACTCGGACTGGACGGCTAT
                                                                                                                                              285
                                                                                                                                                                                                                                                                                                                                                                                                                      entry and computer-readable M.Irwin, 01-MAR-1990.
                                                                                                                                                                                                                    /protein_id="AAA31558:1"
/protein_id="AAA31558:1"
/db_xref="GI:165966"
/translation="KVFERCELARTLKELGLDGYKGVSLANWLCLTKWESSYNTKATN
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QGITANYAWKSHCRDHDVSSYVEGCSL"
                                                                                                                                            /note="PCR primer"
145 c 182 g
                                                                                                                                                                                                                                                                                                                                                    /organism="Ovis aries"
/db_xref="taxon:9940"
                                                                                                                                                                                       /product="lysozyme 1b"
                                                                                                                                                                                                                                                                                                       /codon_start=
                                                                                                                                                                                                                                                                                                                      /note="lysozyme 1b precursor"
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                                                                            96.4%;
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1 (bases 1 to 881)

1 (bases 1 to 881)

1 (rwin,D.M. and Wilson,A.C.
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Sheep lysozyme lc (lyzlc) mRNA,
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                  AAGGTCTTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTTGGACTGGACGGCTAT: 114
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 AAGGTCTTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGGAACTCGGACTGGACGGCTAT 60
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                                                             Conservative
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                                                                                                                                            /note="PCR primer"
144 c 183 g
                                                                                                                                                                          /product="lysozyme lc"
1. .17
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                                                                                                                                                                                                                                                                                                                     /note="lysozyme 1c precursor"
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                                                            Score 367.6; DB 4
Pred. No. 1.6e-90;
0; Mismatches 14
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pe
Bovidae; Caprinae; Ovis.

1 (bases 1 to 881)
1 rwin, D.M. and Wilson, A.C.
Concerted evolution of ruminant stomach lysozymes.
of lysozyme cDNA clones from sheep and deer
J. Biol. Chem. 265 (9), 4944-4952 (1990)
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Sheep abomasum, cDNA to mRNA.
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Sheep lysozyme 2a (lyz2a) mRNA,
M32495 J05279
                                                                                                                                                                                                                                                                                                                                          Draft entry and computer-readable sequence by D.M.Irwin, 01-MAR-1990.
                                                                                                                                                                                                                                                                                                                                                                                    90202968
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 AAAGCTACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAAC
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96.4%;
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                                                   Score 367.6; DB 4; Pred. No. 1.6e-90; 0; Mismatches 14;
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M32492 J05279
M32492.1 GI:165963
                                                                                                                                                                                                                                                                                                                                                                                         Irwin, D.M. and Wilson, A.C.
Concerted evolution of ruminant stomach lysozymes.
of lysozyme cDNA clones from sheep and deer
J. Biol. Chem. 265 (9), 4944-4952 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec Bovidae; Caprinae; Ovis.
1 (bases 1 to 881)
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                                                               Score 366; DB 4;
Pred. No. 4.5e-90;
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ted: July 5, 2003, 06:13:47 33 secs	Search completed: July Job time : 1383 secs	Sea Job
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TGCAGCGAATTAATGGAAAATAACATCGCTAAAGCTGTAGCATGTGCAAAGCATATTGTC 300	241 Te	ДΔ
TGCAGCGAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTC 354	295 TG	Qy
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AAGGGAGTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACA 120	61 AA	DЬ
AAGGGAGTCAGCCTGGCAAACTGGTTGTTTTGACCAAATGGGAAAGCAGTTATAACACA 174	115 AA	Qy

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Minimum DB seq length: 0
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         987654
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444
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Gapop 10.0 , Gapext 1.0
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23: \SIDS2\gcgdata\geneseq\geneseq-embl\NA1995.DAT: *
24: \SIDS2\gcgdata\geneseq\geneseq-embl\NA2001b.DAT: *
25: \SIDS2\gcgdata\geneseq\geneseq-embl\NA2001b.DAT: *
26: \SIDS2\gcgdata\geneseq\geneseq-embl\NA2001b.DAT: *
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Copyright (c) 1993 - 2003 Compugen Ltd.
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5585.962 Million cell updates/sec
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                                                                                     Sequence encoding p1044-BoLys plasmi Bovine Lysozyme c2 ss sequence of cDN Bovine lysozyme c
                                                                                                                                                                                                                                                                                                                 Description
                             Human benign prost
Sequence encoding
                                                                                                                                                                                                                                                   Bovine lysozyme DN
coding for the
ARBSULT 1
ARAD39128
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AAD39128
AC AAD3
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DE BOVi
XX BOVi
XX BOVi
XX BOVi
XX BOVi
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Mutant human lysoz	AA052670	14	396	35.2	156.2	5
Human colon cancer	ABQ58989	24	706	35.4	157	44
pPLHLY-2 human lys	AAN81735	9	427	35.4	57	3
TaqI - XhoI fragme	AAN92359	10	394	35.4	57	42
ന	AAN81447	9	394	35.4	57	41
Modified DNA seque	AAN81284	9	394	35.4	157.2	40
	AAN81354	9	394	35.4	57	39
Sequence of Tag I-	AAN60214	7	394		157.2	38
Synthetic human ly	AAN70537	œ	418		157.8	37
Sequence encoding	AAN60953	7	418		57	36
Human lysozyme. H	AAQ52669	14	396	36.6	162.6	<u>ω</u>
Human lysozyme gen	AAQ06558	11	396		162.6	34
Sequence of natura	AAN90966	10	396		162.6	ω ω
Human lung tumour	ABK16005	24	233		163.6	32
Sequence of synthe	AAN60206	7	390		163.8	31
Human lysozyme cod	AAI64878	22	390		169.6	30
Mutant human lysoz	AAQ03795	11	399		175.4	29
Avian lysozyme sig	AAQ13590	12	444		176.2	28
Human lysozyme DNA	AAN90102	10	447		176.6	27
Synthetic human ly	AAQ10356	12	464		185.4	26
Human colon tumour	ABL38017	24	585	41.8	185.6	25
Synthetic human ly	AAQ03794	11	449	42.3	187.8	24
Nucleotide sequenc	AAF55437	22	614		222.6	23
Sequence encoding	AAN70944	8	390		239	22
Human colon cancer	AAA16339	21	657		250	21
DNA encoding novel	AAS66076	23	1798		•	20
Human macrophage-e	AAD17740	22	444			19
Human lung-specifi	AAD39104	24	2467	59.7	•	18
Human colon tumour	ABL37496	24	481	60.3	٠	17
Sequence encoding	AAN70943	œ	447	60.6	٠	16
Sequence of human	AAN92054	10	435	60.6	269.2	15
Sequence encoding	AAN70949	æ	490	60.9	•	14
Pancreas cancer re	ABL70110	24	748		~	ü
Human prostate exp	ABV24794	23	1776	63.2	08	12
DNA encoding novel	AAS65881	23	1512	63.2	0	11
Human macrophage-e	AAD17725	22	1512	63.2	280.6	10

ALIGNMENTS

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AAD39128
ID AAD39128;
XX
AC AAD39128;
XX
AC AAD39128;
XX
BOVine lysozyme DNA.
XX
BOVine; viral vector; transgenic plant; lysozyme; antibacterial;
KW plerce's disease; PD; Xylella fastidiosa bacterium infection;
KW anti-Xylella reagent; grapevine; gene; ds.
XX
OS Bos sp.
XX
FH Key
FT CDS

A*tag= a
FT
XX
PD

25-APR-2002.
XX
PD

25-APR-2002.
XX
PD

25-APR-2001; 2001WO-US32147.
XX
PR

XX
PR

18-OCT-2000; 2000US-240967P.
XX
PPA

(LARG-) LARGE SCALE BIOLOGY CORP.
XX
POgue G, Velichko S;
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RESULT 2
AAQ05054
ID AAQ0
XX
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to viral vectors and methods for producing transgenic plants that express heterologous DNA that encode a ruminant lysozyme, preferably bovine. This lysozyme protects against diseases caused by plant pathogens particularly bacterial pathogens. The method is useful for producing bovine lysozyme in host plants e.g. grapevines. Plasmid encoding a recombinant plant virus which comprises a bovine lysozyme encoding nucleic acid, is useful for producing bovine lysozyme encoding nucleic acid, is recombinant source of BoLys protein for producing bovine lysozyme protein which acts as an anti-Xylella reagent for development of a recombinant source of BoLys protein for treating grapevines against Pierce's disease (PD). The method is useful for protecting grapevines against Xylella fastidiosa bacterium infection that causes PD. The present sequence is bovine lysozyme DNA.
              Sequence encoding bovine lysosyme
                                              30-OCT-1990
                                                                           AAQ05054
                                                                                                          AAQ05054 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 444 BP; 128 A; 86 C; 117 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing bovine lysozyme (BoLys) in plants e.g. grapevines, useful for protecting grapevines against Pierce's disease by infecting host plant with recombinant virus containing nucleic acid encoding BoLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAE24348
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                                                                                                                                                                                                                  TACGTTGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                                               CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT
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                                             (first entry)
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Best Local
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the cell to produce bovine lysosyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 459 BP; 132 A; 89 C; 119 G; 119 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence may be inserted into the DNA of Pichia pastoris at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel DNA fragments comprising Pishia pastoris GAPDH gene it's 5'-regulatory region and 3'-transcription termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 10; Table 2; 26pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAPDH; Glyceraldehyde-3-phosphate dehydrogenase;
additive homogenous recombination; bovine lysosyme c2;
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                        421
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            TACGTTGAGGGTTGCACCCTGTAA 444
                                                                CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGAGCCATGACGTCAGCAGT
                                                                                                                    GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
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TACGTTGAGGGTTGCACCCTGTAA
                                                   CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT
                                                                                                      GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                                                                                                                                                                                                          ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 240
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                                                                                                                                                                                                            ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                                                                                                                                                                                                                                                         GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAAGCT 180
                                                                                                                                                                                                                                                                                                                  TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA
                                                                                                                                                                                                                                                                                                                                                                     ATGAAGGCTCTCGTTATTCTGGGGGTTTCTCTTTCTGTCGCTGTCCAAGGCAAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88US-0289357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89EP-0123652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disrupting the gene activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 444; DB 11;
Pred. No. 3.4e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
450
                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 459;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transforming
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                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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                                                                             420
                                                   426
                                                                                                      366
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                                                                                                                                                                                   300
                                                                                                                                                                                                             246
                                                                                                                                                                                                                                                                 186
                                                                                                                                                                                                                                                                                                                    126
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RESULT 3
AAD39129
ID AAD3

AAD39129

standard; DNA; 10130 BP

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                                                                                                                                                                                                                                           Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                         The invention relates to viral vectors and methods for producing transgenic plants that express heterologous DNA that encode a ruminant lysozyme, preferably bovine. This lysozyme protects against diseases caused by plant pathogens particularly bacterial pathogens. The method is useful for producing bovine lysozyme in host plants e.g. grapevines. Plasmid encoding a recombinant plant virus which comprises a bovine lysozyme encoding nucleic acid, is useful for producing bovine lysozyme protectin which acts as an anti-Xylella reagent for development of a recombinant source of BoLys protectin for treating grapevines against tylella fastidiosa bacterium infection that causes PD. The against systella fastidiosa bacterium infection that causes PD. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine; viral vector; transgenic plant; lysozyme; antibacterial; Pierce's disease; PD; Xylella fastidiosa bacterium infection; anti-Xylella reagent; grapevine; cyclic; circular; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Producing bovine lysozyme (BoLys) in plants e.g. grapevines, useful for protecting grapevines against Pierce's disease by infecting host plant with recombinant virus containing nucleic acid encoding BoLys -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p1044-BoLys plasmid DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Fig 2; 36pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-OCT-2000; 2000US-240967P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200233041-A2
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                                                                                                                                                                                                                                                                                                   Sequence 10130 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-OCT-2001; 2001WO-US32147
                                                                                                                                                                                                                                                                                                                                              present sequence is p1044-BoLys plasmid DNA containing bovine lysozyme
                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                               5767
                                                                                                                   5827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002-479667/51.
                            181
                                                                                                                                                                                                                                         444;
                                                                                      121
                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LARGE SCALE BIOLOGY CORP
                                                     TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA
                                                                                                                                                                               ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
              ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                                                                                                                 TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA
                                                                                                                                                                                                             ATGAAGGCTCTCGTTATTCTGGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Velichko S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Bovine lysozyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                             2854 A; 2078 C; 2492 G; 2706 T; 0 other;
                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                      Score 444; DB 24;
Pred. No. 1.2e-126;
                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                     Length 10130;
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6006
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RESULT 4
AAV08922
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                                                                                                                                                                                                                                                                       12-JAN-1995;
19-SEP-1991;
25-NOV-1991;
22-APR-1997;
                                 used in the transgenic plant of the invention. The transgenic plant is resistant to plant pathogens and contains heterologous DNA encoding a ruminant or ruminant-like lysozyme, the plant expresses sufficient levels of the lysozyme to render it less susceptible to the pathogens than the wild-type plant. The plants are resistant to bacterial pathogens such as
                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine Lysozyme c2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV08922 standard;
                                                                                                 This sequence encodes the bovine lysozyme c2 and can be
                                                                                                                          Example 1; Column 37-40; 23pp; English.
                                                                                                                                                           Transgenic plants resistant to bacterial pathogens - contain
                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                       Fitzmaurice LC,
                                                                                                                                                                                                                                                                                                                                     22-APR-1997;
                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                    US5850025-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathogen resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lysozyme; signal peptide; transgenic plant; plant pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV08922;
Sequence 964 BP; 297 A; 165 C; 201 G; 301 T; 0 other;
                       Pseudomonas syringae or Erwinia carotovora.
                                                                                                                                                                                                                                                (SIBI-) SIBIA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6187
                                                                                                                                                                                               1999-069855/06
                                                                                                                                                                                      AAW73502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACGTTGAGGGTTGCACCCTGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGTGGTGTAATGATGGCAAAACCCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                       95US-0373390.
91US-0762679.
91US-0798223.
97US-0919093.
                                                                                                                                                                                                                                                                                                                                     97US-0919093
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
25..462
/*tag= a
                                                                                                                                                                                                                         Mirkov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coding sequence
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Query Match Best Local Si Matches 439;

Similarity

98.9%; Su 100.0%; Pr 0;

Score 439; DB 20; Pred. No. 1.6e-125;

Length 964; indels

0; Gaps

0;

Mismatches

Conservative

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RESULT 5
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   (SALK ) SALK
                   02-NOV-1987;
                                    02-NOV-1988;
                                                     18-MAY-1989
                                                                                             3'UTR
                                                                                                            mat_peptide
                                                                     WO8904320-A
                                                                                                                                                      misc_feature
                                                                                                                                                                                                       Bovine
                                                                                                                                                                                                                             Bovine lysozyme C2; protein signal sequence; Pinchia pastoris
                                                                                                                                                                                                                                                ss sequence
lysozyme C2
                                                                                                                                                                                                                                                                        07-APR-1990
                                                                                                                                                                                                                                                                                        AAN92057;
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                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                 444
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                                                                                                                                                                                                                                                                                                                                                          TGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                                                                                                                                                                               CATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGTTACGT
                                                                                                                                                                                                                                                                                                                                                                                          CATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGTTACGT
                                                                                                                                                                                                                                                                                                                                                                                                                AATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAGCAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGTAATGATGCCAAAACCCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTGGCAAACTGGTTTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAA
                                                                                                                                                                                                                                             of cDNA insert of clone lambda BL3 encoding bovine together with 3' untranslated region.
   INST FOR BIOL STUD.
                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                       protein
                    87US-0115940.
                                   88WO-U503907
                                                                                                    /*tag= c
68..462
/*tag= d
                                                                                             /*tag= c
463..964
                                                                                                                                                      /standard_name=
942..964
                                                                                                                             /standard_name=
25..462
                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                              "EcoRI
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RESULT 6
AAQ39092
ID AAQ3
XX
AC AAQ3
XX
DT 20-J
XX
BOV1
XX
BOV1
KW Gram
KW Gram
KW Agro
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                Matches
       Bovine; lysozyme c; transgenic; plant; resistance; pathogen; gram negative; bacteria; hen egg white lysozyme; potato; tobacc tomato; carrot; apple; sunflower; petunia; violet; Pseudomonas; Agrobacterium; Xanthomonas; Erwinia; Clavibacter; ss.
                                                 Bovine lysozyme c DNA.
                                                                  20-JUL-1993
                                                                                  AAQ39092;
                                                                                                  AAQ39092 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino-terminus of the mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Digan ME, H
Williams ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pages 26-29; ; 85pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1989-165613/22
                                                                                                                                            444
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                                                                                                                                                                                                             324
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                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                 (first entry)
                                                                                                   DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                      98.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                   964
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                                                                                                  ВP
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                                                                                                                                           462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thill
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The 3'-noncoding sequence does not contain a polyadenylation signal or a poly (A)+ tail. The 5'-terminus does not contain the ATG triplet corresponding to the translation initiation codon fo the pre-lysozyme C2 mRNA. Thus the cDNA insert encodes 16 amino acids amino-terminal to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 964 BP; 298 A; 165 C; 200 G; 301 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prodn. of animal lysozyme C from pichia pastoris by secretion consists of P. pastoris promoter and terminator DNA
CATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGTTACGT 425
                                                                                                                                                                                                                                                                                  CTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTG
                                                                                                                                                                                                                                                                                                                                                                               CCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAA 185
                                                                                                                       AATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAGCAAGG
                                                                                                                                                                                                                      GTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG
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                                                                                              AATGGAAAATGACATCGCTAAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAGCAAGG
                                                                                                                                                                                           GTGTAATGATGCCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACTCTCGTTATTCTGGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 437.4; DB 10;
Pred. No. 5e-125;
0; Mismatches 1;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the production of transgenic plants that are resistant to pathogens. The lysozyme encoded by this sequence has a greater ability to lyse gram negative bacteria than hen egg white lysozyme and also has a greater stability. The lysozyme may be applied directly to treat or protect plants such as potatoes, tobacco, tomatos, carrots, apples, sunflowers, petunias and violets from plant pathogens such as Pseudomonas, Agrobacterium, Xanthomonas, Erwinia and Clavibacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protection of plants against plant pathogens - by transforma with DNA encoding a ruminant or ruminant like lysozyme, esp. bovine lysozyme C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 73-74; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-SEP-1991;
25-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence encodes bovine lysozyme {f c} . This sequence was used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMAR-) SMART PLANTS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          taurus.
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 426
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                             GTGTAATGATGGCAAAACCCCTAATGCAGTTĆACGGCTGTCATGTATCCTGCAGCGAATT 305
                                                                                                                                                                                                            CTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTG
                                                                                                                                                                                                                                          CTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTG 245
                                                                                                                                                                                                                                                                        CGTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAA 203
                                                                                                                                                                                                                                                                                                    CCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAA 185
                                                                                                                                                                                                                                                                                                                                   GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGCGAGTCAG
                                                                                                                                                                                                                                                                                                                                                 GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG 125
                                                                                                                                                                                                                                                                                                                                                                                          GGCTCTCGTTATTCTGGGGGTTTCTCTTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             964 BP; 297 A; 165 C; 201 G; 301 T; 0 other;
TGAGGGTTGCACCCTGTAA 444
                                                           CATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGGACCATGACGTCAGCAGTTACGT 425
                                                                                                                     AATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAGCAAGG 365
                                                                                                                                                 GTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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91US-0798223.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 435.8; DB 14
Pred. No. 1 6e-124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 14; Length 964;
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1 ATGAAGGCTCTCGTTATTCTGGGGTTTCTTCTTTCTGTCGCTGTCCAAGGCAAGGTC

ATGAAGGCTCTCATTGTTCTGGGGCTTGTCCTCCTTTCTGTTACGGTCCAGGGCAAGGTC

73

Matches

ocal

Similarity

63.2%; 78.3%;

Score 280.6; DB 24; Mismatches No. 1.8e-76; smatches 94;

Conservative

0 Pred.

Indels Length 1483;

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Sequence 1483 BP; 432 A; 298 C; 309 G; 444 T; 0 other;

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                       The invention relates to a method of diagnosing (I) the onset or cc progression of benign prostatic hyperplasia (BPH), or screening (II) for cor identifying an agent that modulates the onset or progression of BPH.

CC The method is based on changes in gene expression in BPH tissue isolated crom patients exhibiting different clinical states of prostate compared to normal prostate tissue. (I) comprises compared to normal prostate tissue. (I) comprises composed to normal prostate tissue. (I) comprises preparing a first gene expression profile configuration as econd gene expression profile of the agent exposed configuration and comparing the first and second gene expression profiles. (I) susful for identifying an agent that modulates the onset or progression configuration for level in a tissue or cells, by comparing the expression of BPH. (II) is configurated to fix the expression level in a tissue or cells, by comparing the expression configuration in the tissue or cells to the compared to the expression of gene in the database, and displaying the compared to the expression level in BPH. Agents using (II) are useful for treating BPH or prostate cancer. ABK64106-ABK6480 represent human configuration prostatic hyperplasia gene sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying drugs for and diagnosing benign prostatic hyperplasia, by detecting expression levels of one or more genes in prostate cells from patient that are differentially regulated compared to normal prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-AUG-2000;
05-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 241; 444pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Munger WE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; benign prostatic hyperplasia; BPH; prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENE-) GENE LOGIC INC.
(NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-FEB-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   benign prostatic hyperplasia gene #412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kulkarni P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-223323P
2001US-0873319
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RESULT 8
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                                                Human lysozyme DNA can be used to obtain transgenic animals, e.g. mice. It can also be produced by culturing animal cells, and it can promote the genetic expression of these animal cells.
Sequence 1494 BP; 441 A; 298 C;
                                                                                                                                                                                                 Human lysozyme gene -
useful promoter for genetic expression of animal culturing
                                                                                                                                                                                                                                                                                                                                    WPI; 1990-053916/08.
                                                                                                                                                                                                                                                                                                       P-PSDB; AAR06108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP02005879-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic animal; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence encoding human lysozyme
                                                                                                                                                                                                                                                                                                                                                                                       (TAKE ) TAKEDA CHEMICAL IND KK
                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUN-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JAN-1990
                                                                                                                                                         Fig 4-1 to 4-3 Pages 834-835; 13pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCACAAGGCATTAGAGCATGGGTGGCATGGAGAAATCGTTGTCAAAACAGAGATGTCCGT 433
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68..460
/*tag= b
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309 G; 446 T; 0 other;
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RESULT 9
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ID AAN92386
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Best Local
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                       P-PSDB; AAP93510.
                                                WPI; 1989-127529/17.
                                                                                                                                                                                                                                                                                               JP01074989-A
                                                                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
                                                                                                                                               16-SEP-1987;
                                                                                                                                                                                                16-SEP-1987;
                                                                                                                                                                                                                                                 20-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human lysozyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAN92386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAN92386 standard; DNA; 1496
                                                                                              (TAKE ) TAKEDA CHEMICAL IND KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         434 CAGTATGTTCAAGGTTGTGGAGTGTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGAAGGCTCTCGTTATTCTGGGGGTTTCTTCTTTCTGTCGGTGTCCAAGGCAAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GCAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGA- 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAACTTGGACTGGACGGCTATAAGGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTTACGTTGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCACAAGGCATTAGAGCATGGGTGGCATGGAGAAATCGTTGTCAAAACAGAGATGTCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTTTGCTGCAAGATAACATCGCTGATGCTGTAGCTTGTGCAAAGAGGGGTTGTCCGTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCAGCCTAGCAAACTGGATGTGTTTGGCCAAATGGGAGAGTGGTTACAACACACGAGCT
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                                                                                                                                               87JP-0229752
                                                                                                                                                                                                87JP-0229752
                                                                                                                                                                                                                                                                                                                                             /*tag=
14..460
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
68..457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 14..67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 signal peptide and mature protein of human lysozyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.2%;
78.3%;
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Pred. No. 1.8e-76;
0; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460
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RESULT 10
AAD17725
ID AAD17725
AC AAD17
XX AD17
XX IO-DE
XX Human
XX Human
XX Human
XX Gene
KW Human
XW Gene
KW Gene
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KW Alzhe
KW Alzhe
KW Lhrom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       It is useful for effective expression of human lysozyme in yeast or animal cells. Also, DNA encoding various proteins can be linked to the 3' end of the HL signal peptide so that it is downstream of the promoter of the expression vector. Expression of such proteins is possible in E. coli, Bacillus subtilis, yeast or animal cells. Lysozyme
Human; macrophage-expressed protein; inflammation; angiogenesis; cancer; transplantation; myelodysplastic syndrome; transgenic animal; ischaemia; gene therapy; Crohn's disease; immune disorder; myeloid leukaemia; shock; sepsis; nephritis; genetic disorder; nervous system disease; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; fibrosis; amyotrophic lateral sclerosis; lymphoid cell disorder; platelet disorder; thrombocytopenia; osteoarthritis; bone degenerative disorder; thrombosis; periodontal disease; osteoprosis; tissue repair; burn; incision; ulcer; multiple sclerosis; rheumatoid arthritis; allergy; asthma; thrombolysis; coagulation disorder; hereditary disorder; haemophilia; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1496 BP; 443 A; 299 C; 308 G; 446 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding signal peptide and mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New DNA sequence -
                                                                                                                                                                                                                                                                                                                                               10-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD17725 standard; cDNA; 1512 BP
                                                                                                                                                                                                                                                                                               Human macrophage-expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for controlling bacterial infection and unlike chicken lysozyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2-1 - 2-1; pages 12-13; 13pp; Japanes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGTGGTGATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCACAAGGCATTAGAGCATGGGTGGCATGGAGAAATCGTTGTCAAAACAGAGATGTCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTTTGCTGCAAGATAACATCGCTGATGCTGTAGCTTGTGCAAAGAGGGGTTGTCCGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACTGGTGTAATGATGGCAAAACCCCAGGAGCAGTTAATGCCTGTCATTTATCCTGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAAACTACAATGCTGGAGACAGAAGCACTGATTATGGGATATTTCAGATCAATAGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCAGCCTAGCAAACTGGATGTGTTTGGCCAAATGGGAGAGTGGTTACAACACACGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGAAGGCTCTCATTGTTCTGGGGCCTTGTCCTCCTTTCTGTTACGGTCCAGGGCCAAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --GCAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.2%;
                                                                                                                                                                                                                                                                                                    cDNA #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 280.6;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8e-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of human lysozyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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antidiabetic;
                                                                                                            antibacterial; immunosuppressive; analgesic; vulnerary; immunostimulant;
vaccine; vasotropic; nootropic; haemostatic; osteopathic; fungicide;
sapiens
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Homo

mat_peptide sig_peptide /*tag= b 83..472 /*tag= c /product= /product= 29..82 /*tag= location/Qualifiers ρ "Human "Human macrophage-expressed protein" mature macrophage-expressed protein"

WO200164839-A2

28-FEB-2001; 2001WO-US06475

31-MAR-2000; 11-DEC-2000; 28-FEB-2000; ; 2000US-0515126. ; 2000US-0540217. ; 2000US-0255200.

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(HYSE-) HYSEQ INC

Dickson Dedera D, Boyle BJ, ⊔ Labat Liu ĊΉ Stache-crain Tang YT; В,

P-PSDB; AAE10577 2001-582152/65.

Novel macrophage-expressed nucleic acids and polypeptides for diagnosis and treatment of inflammatory, autoimmune, neurological, myeloid or lymphoid cell disorders, cancer and for promoting wound healing

Claim 1; Page 139-140; 158pp; English.

CC differentiation and survival of pluripotent and totipotent stem cells call differentiation and survival of pluripotent and totipotent stem cells co differentiation and survival of pluripotent and totipotent stem cells co differentiation and survival of pluripotent and totipotent stem cells co differentiation and survival of pluripotent at the protein is used to manipulate stem cells in culture to give rise to concurre protein is used to manipulate stem cells in culture to give rise to concurre protein is used to manipulate stem cells in culture to give rise to concurre the treatment of protein culture to give rise to by illness, accidental damage or genetic disorders, induces the concurred concurred the treatment of central and peripheral nervous system conditions and neuropathies, such as Alzheimer's, Parkinson's disease, concurred the treatment of central and peripheral nervous system constanting lymphoid cell disorders; platelet disorders such as thrombocytopenia and osteoporosis, osteoarthritis, bone degenerative disorders or periodontal disease and for regeneration of bone, cartilage, constant and ligament and in tissue repair, healing of burns, incisions considered the constant protection, treatment constant protection and disorders such as severe combined immunodeficiency (SCID), bacterial or fungal infections, cartilage, constant protection as asthma or other respiratory problems and is involved in thrombolysis or thrombosis is useful in treatment of coagulation and other haemostatic events in treatment of coagulation constants and the respiratory problems and is involved constants. Fertility of male or female subjects, incisions, fertility of male or female subjects, and constants respectively. reperfusion injury, shock, sepsis, immune responses, cancer and myeloid leukaemia and myelodysplastic syndromes. The protein exhibits activity relating to angiogenesis, cytokine, stem cell growth factor activity and transgenic animals. Macrophage-expressed molecule is useful treating The present invention relates to an isolated macrophage-expressed cDNA inflammatory conditions such as nephritis, Crohn's disease, ischaemiaits protein. The invention is used in gene therapy and in creating of male temale subjects,

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RESULT 11
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23-AUG-2000;
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                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                    30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                       11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding novel human diagnostic protein #1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-2002 (first entry)
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   Liu C,
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2000US-0649167
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC in identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity cand to produce other types of data and products dependent on DNA and CC amino acid sequences ASS64197-AAS9454 represent novel human cc diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed content of the p
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AGTTACGTTGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                           GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGA- 359
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                                                                CACAAGGCATTAGAGCATGGGTGGCATGGGAGAAATCGTTGTCAAAACAGAGATGTCCGT
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                                                                                                                      --GCAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGC 417
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Best Local Similarity
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 4747-4748; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful
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09-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1776 BP; 523 A; 368 C; 390 G; 492 T; 3 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΑBV24794;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is also useful as a pharmacodyanamic or pharmacogenomic marker.
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                         TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120
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Pred. No. 2e-76;
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RESULT 13
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cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --GCAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGTATGTTCAAGGTTGTGGAGTGTAA
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2000US-234017P.
2000US-234034P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical CC agent to be tested for anti-neoplastic activity, determining a change in CC expression of at least one gene (I) of a signature gene set, where (I) CC comprises a sequence (S) selected from 8447 sequences (given in ABL6164 CC to ABL70110), or is at least 95% identical to (S), where a change in CC expression is indicative of anti-neoplastic activity. (I) has cytostatic CC extivity and can be used in gene therapy. MI can be used for screening CC an anti-neoplastic agent, and can be used for product which CC is the data collected with respect to the anti-neoplastic agent as a CC result of M1, and the data is sufficient to convey the chemical CC structure and/or properties of the agent. MI can be used in the CC comparation and can be used in the CC comparation and conversation convey the chemical CC comparation and conversation conversation can be used in the CC comparation and conversation conversation can be used in the CC comparation and conversation conversation can be used in the CC comparation according to the conversation can be used in the CC comparation and conversation or pancreatic cancer.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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03-OCT-2000;
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GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGA-
                                                                                                                                                                                                                                TACTGGTGTAATGATGGCAAAACCCCAGGAGCAGTTAATGCCTGTCATTTATCCTGCAGT
                                                         TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
                                                                                                                                                                                    GTCAGCCTGGCAAACTGGTTGTGTTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT
                                                                                                                                                                                                                                                                                            ACAAACTACAATGCTGGAGACAGAAGCACTGATTATGGGATATTTCAGATCAATAGCCGC
                                                                                                                       ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                                                                                                                                     ATGAGCCTAGCAAACTGGATGTGTTTGGCCAAATGGGAGAGTGGTTACAACACACGAGCT
                                                                                                                                                                                                                                                                TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                     748 BP; 215 A; 138 C; 169 G; 226 T; 0 other;
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2000US-237294P.
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2000US-23731SP.
2000US-237425P.
2000US-237568P.
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2000US-237173P.
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78.1%;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 490 BP; 122 A; 100 C; 149 G; 119 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New hybrid plasmids contg. sequences for human lysozyme - useful e.g. as antiviral and antibacterial agent, and transformed hosts {\sf e}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 4; 18pp; German
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                                                                                                                                                                                                                                                                                                                                                                              Local
128 TGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAAACT
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                                                                                                                          68 GATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAGCC
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                                                                                   8 CTCTCGTTATTCTGGGGTTTCTCTTCTTCTGTCGCTGTCCAAGGCAAGGTCTTTGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGTATGTTCAAGGTTGTGGAGTGTAA
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77.5%;
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                                                                                                                                                                                                                                                                                                                                                                        Score 270.4; DB 8; Pred. No. 1.7e-73;
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                       amino acids, it encodes the entire sequence of human pre-lysozyme C of placental origin in addition to a translational stop signal. The mature lysozyme C corresponding to the pre-lysozyme C encoded by AAN92054 has the same AA sequence as human milk lysozyme. AAN92054 differs from the nucleotide sequence of the cDNAs encoding human pre-lysozyme C isolated from human histlocytic lymphoma cell line|U-937 (see FT tags a and b). However, these nucleic acid differences do not alter the amino acid
                                                                                                                                                                                                                                                                                                                                                                 Prodn. of animal lysozyme C from pichia pastoris by secretion consists of P. pastoris promoter and terminator DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-NOV-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of human pre-lysozyme C of placental origin.
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                                                                                                                                                                                                                          Sequence contained in plasmid pHLZ100. Apart from the four N-terminal
                                                                                                                                                                                                                                                                                  Page 56; ; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Williams ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-MAY-1989
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

	JOURNAL COMMENT	TITLE	AUTHORS	REFERENCE		ONGENERAL	ORGANTSM	KEYWORDS	VERSION	ACCESSION	LOCUS DEFINITION	RESULT 1 BG937925
Beef Genomics Laboratory Dept of AFNS, University of Alberta 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada Tel: 780 492 0169 Fax: 780 492 4265 Email: smoore@afns.ualberta.ca The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA) in main database at high score of 898.0 and E-value of 0.0 PCR PRIMERS FORWARD: M13 Forward BACKWARD: M13 Reverse	Unpublished (2001) Contact: Dr. Stephen Moore	cDNA's from bovine abomasum tissue	Moore, S.S., Hansen, C., Li, C., Fu, A., Meng, Y. and Li, G.	Bovidae; Bovinae; Bos. 1 (bases 1 to 453)	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;	Fukarvota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;	Ros taurus	EST.	BG937925.1 GI:14337297	sequence. BG937925	13bo09H04 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA	

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                                                                                                                                                                            sequence.
BG938107
MOORE,S.S., Hansen,C., Li,C., Fu,A
CDNA's from bowine abomasum tissue
Unpublished (201)
Contact: Dr. Stephen Moore
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                                                                       Bovidae; Bovinae; Bos.
                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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/lab_host="XIJ-BlueMRF'.strain"
/note="Organ: Abomasum; Vector:
1; Site_2: Xho I"
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/sex="Two males and one female mixed"
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/cell_type="Epithelial"
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Pred. No. 4.9e-125;
); Mismatches 0;
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                                          Meng, Y.
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sequence. BG938377 BG938377.1

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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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Seg primer: T3 primer
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High quality sequence stop:
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/note="Organ: Abomasum; Vector:
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/dev_stage="Young adult"
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Pred. No. 4.9e-125;
Mismatches 0;
                  463 bp
 cDNA Library Bos
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421 TACGTTGAGGGTTGCACCCTGTAA 444
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Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of APNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moore, S.S., Hansen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA) in main database at high score of 918.0 and E-value of 0.0
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                                                 CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT 420
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                                                                                                         GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGCAAAGCATATTGTCAGTGAG
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/ceil_type="Epithelial" |
/dev_stage="Young adult" |
/lab_host="XLI-BlueMRF'-strain"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: Ecor
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/sex="Two males and one female mixed"
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/db_xref="taxon:9913"
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91 c 119 g
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Pred. No. 4.9e-125;
; Mismatches 0;
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 464)
Moore, S.S., Hansen, C., Li, C., Fu, A., cDNA's from boyine abomasum tissue
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Contact: Dr. Stephen Moore
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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1Abo07G10 Bovine Abomasum
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TGGTGGTGTAATGATGGCAAAACCCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
                  TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
                                                                       ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                                                       ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 240
                                                                                                                                            GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT 193
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/sex="Two males and one female mixed"
/tissue_tpe="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
/dev_stage="Young adult"
/lab_host="XL1-BlueMRF'.strain"
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Pred. No. 4.9e-125;
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410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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Contact: Dr. Stephen Moore
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The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme)_in main database at high score of 930.0 and E-value of 0.0
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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/cell_type="Epithellal"
/dev_stage="Young adult"
/lab_host="XL1-BlueMRF'-strain"
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/sex="Two males and one female mixed".
                                                                                                                                                                                                  /note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: Ecor
I; Site_2: Xho I"
92 c 123 g 121 t
                                                                                                                                                                                                                                                                                                                                           /organism="Bos taurus"
/db_xref="taxon:9913"
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                                                                                                                        Score 444; DB 13;
Pred. No. 5e-125;
); Mismatches 0;
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                                                                                                                          Indels
                                                                                                                                                       Length 469;
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CDNA 5', mRNA
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                                                                                                                       Gaps
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High quality sequence stop:
POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                 Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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1Abo03C3
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                                                                                                                                                                                                                                                                                                                                  Email: smoore@afns.ualberta.ca
The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA)in main database at high score of 944.0 and E-value of 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2001)
Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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Dre,S.S., Hansen,C., Li,C.,
               135
        /dev_stage="Young adult"
/lab_host="XL1-BlueNEF'-strain"
/note="Organ: Abomasum; Vector:
/, Site_2: Xho I"
94 c 122 g 125 t
                                                                                           /tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
                                                                                                                            /db_xref="taxon:9913"
/clone_lib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
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Query Match

100.0%;

Score 444;

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Length 476;

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BG938203
BG938203.1
                                                                                                                                                                               Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                             MOORE, S.S., Hansen,C., Li,C., Fu,A
CDNA's from bovine abomasum tissue
Unpublished (2001)
Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                                                               EST
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1Abo13G08 Bovine Abomasum
                                                                            Seq primer: T3 primer 
High quality sequence
                                                                                                    BACKWARD: M13
                                                                                                                                         The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme ) in main database at high score of 944.0 and E-value of 0.0
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                                                                                                                   FORWARD: M13 Forward
                                                                                                                               PCR PRimers
                                                                                                                                                                     Email: smoore@afns.ualberta.ca
                                                                 POLYA-No
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                                                                                                                                                                                                                                   Beef Genomics Laboratory
                                                                            quality sequence
                                                Location/Qualifiers
            /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="Bovine Abomasum
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BASE COUNT
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              421 TACGTTGAGGGTTGCACCCTGTAA 444
                                                                    378 CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT
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                                                                                       CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT 420
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TACGTTGAGGGTTGCACCCTGTAA
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/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
/dev_stage="Young adult"
/lab_host="XIJ-BlueMRF'.strain"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; S
I; Site_2: Xho I"
93 c 123 g 125 t
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Pred. No. 5e-125;
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Unpublished (2001)
Contact: Dr. Stephen Moore
Deef Genomics Laboratory
Dept of AFNS, University of Alberta
A10 Agrifor, Dept of AFNS, U of A, E
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
BG937601
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The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA) in main database at high score of 948.0 and E-value of 0.0
                                                                                                                                                                                                                    Moore, S.S., Hansen, C., Li, C., Fu, A., cDNA's from bovine abomasum tissue
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EST.
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1Abo03H1 Bovine Abomasum
                                               Email: smoore@afns.ualberta.ca
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ACCESSION
VERSION
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Matches
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                                      Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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    1 (bases 1 Moore, S.S.,
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1Abo07G03 Bovine
                                Bovidae; Bovinae; Bos.
                                                                                           COW
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Seq primer: T3 primer
High quality sequence stop: 478
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FORWARD: M13 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="Young adult"
/lab_host="xil-BlueWRF'-strain"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
I; Site_2: xho I"
95 c 123 g 125 t
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/cell_type="Epithelial"
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/db_xref="taxon:9913"
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   Hansen,C.,
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   Fu,A.,
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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High quality sequence stop:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: smoore@afns.ualberta.ca
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/lab_host="XL1-BlueMRF/-strain"
/note="Organ: Abomasum; Vector:
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/cell_type="Epithelial"
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/sex="Two males and one female mixed"
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Pred. No. 5e-125;
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DEFINITION

BG937936 482 bp mRNA linear EST 11-JUN-2001 lAbo08E01 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA

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REFERENCE
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Unpublished (2001)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmc
Tel: 780 492 0169
Fax: 780 492 4265
Email: Temporator
                                                                                                                                                                                   181 ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 240
                                                                                                                                                                    192
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                                                                                                                                    241 TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC 300
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: smoore@afns.ualberta.ca
The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme )
in main database at high score of 955.0 and E-value of 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovidae; Bovinae;
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                                                                           GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
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/clone_lib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithellal"
/dev_stage="Young adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="XL1-BlueMRF'-strain"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
I; Site_2: Xho I"
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                                          181 ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 240
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1 (Dases 1 to 484)
Moore, S.S., Hansen, C., Li, C., Fu, A., cDNA's from bovine abomasum tissue Unpublished (2001)
Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                             1 ATGAAGGCTCTCGTTATTCTGGGGTTTCTTCTTCTTCTGTCGCTGTCCAAGGCAAGGTC
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410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA) in main database at high score of 959.0 and E-value of 0.0
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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/lab_host="XLI-BlueMRF'-strain"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
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27 c 123 g 128 t
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/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
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/db_xref="taxon:9913"
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AUTHORS
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
                                                                                                                                                                                                                                                                                                                                                                Seq primer: T3 primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Dr. Stephen Moore
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BG938200.1
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                                                                                                                                                                                                                                                                                                                                                                                              FORWARD: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: smoore@afns.ualberta.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia;
                                                                                                                                                                                                                                                                                                                                      POLYA-No.
                             ATGAAGGCTCTCGTTATTCTGGGGTTTCTTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTC
                ATGAAGGCTCTCGTTATTCTGGGGTTTCTCTTTCTTTCTGTCGCTGTCCAAGGCAAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACGTTGAGGGTTGCACCCTGTAA 444
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                                                                                                                                                 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 485)
                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 485
                                                                                                                                               מ
                                                                                                                                                                                                    /tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
/dev_stage="Young adult"
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                         /lab_host="XL1-BlueMRF'-strain"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
                                                                                                                                                                                                                                              /clone_lib="Bovine Abomasum cDNA Library"/sex="Two males and one female mixed"
                                                                                                                                                                                                                                                                            /db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                           /organism≕"Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                 Site_2:
97 c
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                                                                                      100.0%;
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                                                                    Score 444; DB 13,
Pred. No. 5e-125;
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                                                                                                                                                           FEATURES
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                            source
                                                                                                                                                                                                                                                                                                  Moore, S.S., Hansen, C., Li, C., Fu, A., McDNA's from bovine abomasum tissue Unpublished (2001)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta 410 Agri/For, Dept of AFNS, U of A, Edrel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421
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Seq primer: T3 primer
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POLYA=No.
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BG937882
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1Abo09C07 Bovine Abomasum
                                                                                                                                                                                                                                                                                      Email: smoore@afns.ualberta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACGTTGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 486)
                                                     /clone_lib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
/tissue_type="dastrointestinal tissue (GI
/cell_type="Epithelial"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
I; Site_2: Xho I"
                         /dev_stage="Young adult"
/lab_host="XL1-BlueMRF'-strain"
                                                                                                                /organism="Bos taurus"
/db_xref="taxon:9913"
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301 GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
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                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme) in main database at high score of 963.0 and E-value of 0.0 Edmonton, AB, T6G 2P5, 7A mRNA

(GIT)"

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RESULT 14
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                                                                                                                                                       Unpublished (2001)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agriffor, Dept of AFNS, U of A, EG
Tel: 780 492 0169
Fax: 780 492 4265
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1Abol1C10 Bovine Abomasum
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Mammalia; Eutheria; Cetartiodactyla;
                    POLYA-No.
                                                            BACKWARD: M13 Reverse
                                                                                           PCR PRimers
                                                                                FORWARD: M13 Forward
                                                                                                                         The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme
                                                                                                                                         Email: smoore@afns.ualberta.ca
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                                                                                                             in main database at
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                                                 primer: T3 primer
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                                  quality sequence stop: 486
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actyla; Ruminantia; Pec
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                                                                                                                                                                                       Edmonton,
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cora; Bovoidea;
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Moore, S.S., Hansen, C., Li,C., Fu,A., I cDNA's from bovine abomasum tissue Unpublished (2001)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta 410 Agri/For, Dept of AFNS, U of A, Ed
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/dev_stage="Young adult"
/lab_host="XIL-BlueMRF'-strain"
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I; Site_2: Xho I"
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/db_xref="taxon:9913"
/clone_lib="Bovine Abomasum cDNA Library"
/csz="Two males and one female mixed"
                                                                                                                                                       ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 780 492 4265
Email: smoore@afns
                                                 mail: smoore@afns.ualberta.ca
he sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA
in main database at high score of 965.0 and E-value of 0.0
                                                                                                   CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT
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/lab_host="Xil-BlueMEF'-strain"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
I; Site_2: Xho I"
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/db_xref-"taxon:9913"
/clone_lib-"Bovine Abomasum cDNA Library"
/sex-"Two males and one female mixed"
/tissue_type-"Gastrointestinal tissue (GIT)"
/cell_type-"Epithelial"
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2003
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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US-08-89-84 iib-24

US-08-889-84 iib-27

US-08-173-497-1

US-08-286-889-1

US-08-285-618-1

US-08-362-652-1

US-08-605-672-1
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US-08-385-590A-3
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US-09-388-917-1
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US-09-786-023-3
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US-08-32-463-14
US-08-385-590A-1
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Sequence 344, App
Sequent No. 5182195
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US-07-798-223A-1
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                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
STATE: Illinois
                                                                                                             NAME/KEY:
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       Conservative
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Result

98.9%; Score 439; DB 1; Lo 100.0%; Pred. No. 1.5e-133;

Length 964; Indels

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Gaps

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Mismatches

Database

45	44	43	42	41	40	39	38	37	36	35 5	34	33	32	31	30	29	28
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Sequence 3, Appli	Sequence 22, Appl	Sequence 1553, Ap	Sequence 6, Appli	Sequence 7, Appli	Sequence 8, Appli	Sequence 97, Appl	Sequence 97, Appl	•	Sequence 97, Appl	`	`	Sequence 98, Appl	•	Sequence 98, Appl	-	Sequence 98, Appl	Sequence 98, Appl

ALIGNMENTS

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Sequence 1, Application US/07798223A Patent No. 5422108 GENERAL INFORMATION:
                                                                                                                                                                                          APPLICATION NUMBER: US/07/798,22:
FILING DATE: 19911125
CLASSIFICATION: 19911125
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/762,679
APPLICATION NUMBER: 07/762,679
FILLING DATE: 19-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seldman, Stephanie L.
REGISTRATION NUMBER: 33,779
REGISTRATION NUMBER: 51984
TELECOMMUNICATION INFORMATION:
TELEFAX: (619)552-1311
TELEFAX: (619)552-1311
                                                                                                                    TELEFAX: (619)552-0095
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 964 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mirkov, T. Erik
APPLICANT: Fitzmaurice, Leona Claire
TITLE OF INVENTION: Protection of Plants Against Pathogens
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDFASTECT CURRENT APPLICATION DATA:
MOLECULE TYPE: CDNA FEATURE:
                                                 LENGTH: 964 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: double TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 South LaSalle Street, Suite 900
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314

254 253

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GENERAL INFORMATION:

APPLICANT: ENDEGE, WILSON O., ET AL.

TITLE OF INVENTION: WOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: PRODUCTS: II

FILE REFERENCE: CCDNA-260XX

CURRENT APPLICATION NUMBER: US/09/385,982

CURRENT FILING DATE: 1999-08-30

EARLIER APPLICATION NUMBER: 60/328,111

EEARLIER FILING DATE: 1999-06-08

EARLIER FILING DATE: 1999-01-27

EARLIER APPLICATION NUMBER: 60/098,639

EARLIER FILING DATE: 1998-01-27

EARLIER FILING DATE: 1998-08-31

NUMBER OF SEQ ID NOS: 544

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 344

LENCTH: 657
                                                                                                                                                                                      ; NAME/KEY: misc_feature
; LOCATION: (1)...(657)
; OTHER INFORMATION: n = A,T,C
US-09-385-982-344
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US-09-385-982-344
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Patent No. 626233
                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                         Local
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74 AGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAGCCTGGCAA
                                                                  14 TTATTCTGGGGTTTCCTTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGAGAGATGTG
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                                                                                                                      Conservative
                                                                                                                                  56.3%;
                                                                                                             Score 250; DB 4; Le
Pred. No. 5.2e-72;
^ wismatches 97;
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                                                                                                                                                  Length 657;
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; APPLICANT: NAKAHAMA, KAZUO; KE
; TITLE OF INVENTION: METHOD EC
; DEFICIENT YEASTS
; NUMBER OF SEQUENCES: 71
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08,
; ETLING DATE: 09-NOV-1988
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Best Local :
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                                  GTTACGTTGAGGGTTGCACCCTGTAA 444
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               AATACGTTCAAGGTTGTGGTGTTTAA 386
                                                                                CACAGGGTATTAGAGCCTGGGTCGCTTGGAGAAACAGATGCCAAAATAGAGATGTCAGAC
                                                                                                                                                CTTTGCTTCAGGACAACATTGCTGATGCTGTTGCCTGCGCTAAGAGAGTTGTCCGTGACC
                                                                                                                                                                  AATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGA--
                                                                                                                                                                                                                 ATTGGTGTAACGATGGCAAGACTCCAGGTGCCGTCAACGCCTGTCACTTATCTTGCTCAG
                                                                                                                                                                                                                                  GGTGGTGTAATGATGGCAAAACCCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCG
                                                                                                                                                                                                                                                                                                               CAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAAT 241
                                                                                                                                                                                                                                                                                                                                                                   TCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGAGACCATGACGTCAGCAGTTACGTTGA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTC----AGTGAGCAAGGCAT 368
                                                                                                 -GCAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCA 418
                                                                                                                                                                                                                                                                                                                                                   TTTCTTTAGCCAACTGGATGTGTCTTGCTAAGTGGGAATCCGGCTATAACACTAGAGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAZUO;KAISHO, YOSHIHIKO;YOSHIMURA, KOJI
METHOD FOR INCREASING USING PROTEASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 157.2; DB 6; Pred. No. 7.3e-42;
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                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ishige, Fumiharu
TITLE OF INVENTION: Method for enhancing
TITLE OF INVENTION: resistance of plants
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP-165266/1994
FILING DATE: 18-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP-276573/1994
FILING DATE: 11-OCT-1994
ATTORNEY/ACENT INFORMATION:
NAME: SUENSSON, Leonard R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 18-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: IBM DOS Version 5.00 SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                   IDENTIFICATION METHOD: IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
124 AGAGCTACTAACTACAACGCCGGTGACCGTTCTACTGACTACGGTATCTTCCAAATTAAC
                               175 AAAGCTACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAAC 234
                                                                                                      115 AAGGGAGTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACA 174
                                                                                                                                                                                                               250;
                                                                     64 CGTGGTATCTCTTTGGCTAACTGGATGTGTTTTGGCCAAGTGGGAATCTGGTTACAACACT
                                                                                                                                                                          55 AAGGTCTTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTAT 114
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                                                                                                                                          4 AAAGTTTTCGAACGTTGTGAATTGGCCAGAACTTTGAAGAGATTGGGTATGGACGGTTAC 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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110 Gatehouse Road, Suite 500 Eas
                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           nonnatural type
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                                                                                                                                                                                                                                Score 153; DB 1;
Pred. No. 1.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                              synthetic DNA of
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US-08-385-590A-3
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                                                                                                                                  Matches
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                                                                                                                                                      Best
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TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/385,590A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Aldwinckle, Herbert S.
APPLICANT: No. 5824861elli, John L.
TITLE OF INVENTION: TRANSGENIC POMACEOUS FRUIT WITH
                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                             TOPOLOGY: un MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/954,347
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 30,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364 GTGCCTCAATACGTTCAAGGTTGTGTGTCTAA 396
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                                                                                                                                  258;
61 TTTGAGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120
                                                      30 ATGAGGTCTTTGCTAATCTTGGTGCTTTGCTTCCTGCCCCTGGCTGCTCTGGGGGAAAGTC 89
                                                                                          1 ATGAAGGCTCTCGTTATTCTGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTC 60
                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                         586 base pairs
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                                                                                                                                Conservative
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57.7%;
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Pred. No. 2.3e-30;
                                                                                                                                    Mismatches 183;
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US-09-021-520-3
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US-09-021-520-3
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           Query Match
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                                                                                                                                                     TELEFAX: (716) 263-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                       MOLECULE TYPE:
                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 586 base pairs
TYPE: nucleic acid
                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION: (716) 263-1304
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Aldwinckle, Herbert S.
APPLICANT: No. 6100453elli, John L.
TITLE OF INVENTION: TRANSGENIC POMACEOUS FRUIT WITH FIRE
TITLE OF INVENTION: BLIGHT RESISTANCE
                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                           NAME: Goldman, Michael L. REGISTRATION NUMBER: 30,727
                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 14603
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LENGTH: 222
TYPE: DNA
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; ORGANISM: Gallus gallus US-09-388-917-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/388,917
CURRENT FILING DATE: 1999-09-02
EARLIER APPLICATION NUMBER: 10-250619
EARLIER FILING DATE: 1998-09-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hayashizaki, Yosh
TITLE OF INVENTION: Method f
TITLE OF INVENTION: Support
FILE REFERENCE: 1794-0120P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 11-240910 EARLIER FILING DATE: 1999-08-27 NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin
121 GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATG 155
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                                                                                               61 TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120
                                                                                                                                               32 ATGAGGTCTTTGCTAATCTTGGTGCTTTGCTTCCTGCCCCTGGCTGCTCTGGGGAAAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT 180
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                                               TTTGGACGATGTGAGCTGGCAGCGGCTATGAAGCGTCACGGACTTGATAACTATCGGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAAACGGCATGAGCGCGTGGGTCGCCTGGCGCAACCGCTGCAAGGGTACCGACGTCCAG 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCCTGCTGAGCTCAGACATAACAGCGAGCGTGAACTGCGCGAAGAAGATCGTCAGCGAT 386
                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                  14.4%; 63.2%;
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                                                                                                                                                                                                                                                       Score 63.8; DB 4;
Pred. No. 1.6e-11;
0; Mismatches 57;
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0; Mismatches 183;
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Sequence 2, Application US/09388917 Patent No. 6258542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zhao, Yong
APPLICANT: B1, Anding
TITLE OF INVENTION: A NOVEL HUMAN LYSOZYME GENE, ITS ENCODED
TITLE OF INVENTION: POLYPEPTIDE AND THE METHOD FOR PREPARING THEM
FILE REFERENCE: A34053-PCT-USA
CURRENT EPPLICATION NUMBER: US/09/786,023
CURRENT FILING DATE: 2001-06-21
CURRENT FILING DATE: 2001-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-786-023-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/CN99/00131 PRIOR FILING DATE: 1999-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Yu, Long APPLICANT: Fu, Qia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (106)...(552)
NAME/KEY: variation
LOCATION: (79)...(79)
OTHER INFORMATION: A, C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: variation LOCATION: (88)...(8)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 TTGGCTGCCTGGTCACAGGCGCCGAGTCCAAAATCTACACTCGTTGCAAACTGGCAAAAA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 TACAGCCTGGGAAACTGTAAGTCTGTATTCTCATG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 TATTCTCGAGGGCTGGCCTGGACAATTACTGGGGCCTTCAGCCTTGGAAACTGGATCTGCA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 CTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAGCCTGGCAAACTGGTTGTGTT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 TTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGAGAGATGTGAGCTTGCCAGAA 85
                                                                                                                        GCTGGAAGAAACATTGTGAGGGCAGAGACCT
                                                                                                                                                                 CATGGAAAAGTCATTGTCGAGACCATGACGT 413
                                                                                                                                                                                                                                             AAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG---CAAGGCATTACAGCCTGGGTGG 382
                                                                                                                                                                                                                                                                                       TGAAGGAGAACCACCTGCCACGTCGCCTGCTCAGCCTTGATCACTGATGACCTCACAG
                                                                                                                                                                                                                                                                                                                              CTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATTAATGGAAAATGACATCGCTA 325
                                                                                                                                                                                                                                                                                                                                                                      GCATCGACTACGGCATCTTCCAGATCAACACGTTCGCGTGGTGCA---GACGCGGAAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGACCAAATGGGAAAGCAGTTATAACACAAAAĞCTACAAACTACAATCCTAGCAGTGAAA 205
                                                                                                                                                                                                       ATGCAATTATCTGTGCCAGGAAAATTGTTAAAGAGACACAAGGAATGAACTATTGGCAAG
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US-08-232-463-14/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 11-240910 EARLIER FILING DATE: 199-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                           APPLICATION NUMBER: EP 91 1:
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKMER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
  REFERENCE/DOCKET NUMBER: 30 TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE:
                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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les 86; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Alexandria
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1800 Diagonal Road,
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ilarity 66.2%;
Conservative
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Pred. No. 1.9e-06;
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RESULT 11
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INFORMATION FOR SEQ ID NO:
                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                     APPLICANT: Aldwinckle, Herbert S.
APPLICANT: NO. 5824861elli, John L.
TITLE OF INVENTION: TRANSGENIC POMACEOUS FRUIT WITH FIRE
TITLE OF INVENTION: BLIGHT RESISTANCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                               CLASSIFICATION:
   APPLICATION NUMBER:
                                            APPLICATION NUMBER: US/0 FILING DATE: 08-FEB-1995
                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                    CITY: Rochester STATE: New York
                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE:
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                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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                                                                                                                                                                                 New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCAACAGCAAATGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCAT 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACACAAAAGCTACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAG 228
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Clinton Square
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                                                                                                                                                                                                                                             Hargrave,
                                                          US/08/385,590#
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US 07/954,347
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Pred. No. 0.0005;
                                                                                                                                                                                                                                             Devans & Doyle LLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162;
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RESULT 12
US-09-021-520-1
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Best Local Similarity
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                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,520
PRIOR APPLICATION DATA:
                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Aldwinckle, Herbert S.
APPLICANT: No. 6100453ell1, John L.
TITLE OF INVENTION: TRANSGENIC POMACEOUS FRUIT WITH FIRE
                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
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ATTORNEY/AGENT INFORMATION:
                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                       FILING DATE
                     CLASSIFICATION:
                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                              ZIP: 14603
                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                     STREET:
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353 AAAATCACTGTCAACA 368
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DEDNESS: double
                                                                                                                                                                                                                                New York
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                                                                                                                                                                                                                                                               E: Nixon, Hargi
Clinton Square
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48.1%;
                                                                                                                                                                                                                                                                                                                                            BLIGHT RESISTANCE
                                                                                                                                                                                                                                                                                       Hargrave, Devans & Doyle LLF
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30,727
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Pred. No. 0.00048;
0; Mismatches 158;
                                                                                              #1.30
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US-08-449-644-3/c
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Best Local 9
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TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
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REGISTRATION NUMBER: 30,727
REFERENCE,DOCKET NUMBER: 199
TELECOMMUNICATION INFORMATION:
                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE TITLE OF INVENTION: PHOSPHATASE-KAPPA NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                 APPLICANT: Vogel, Wolfgang APPLICANT: Fuchs, Miriam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
 CURRENT APPLICATION DATA:
                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                    STREET: 1155 A
                                                                                                                COUNTRY: UZIP: 10036
                                                                                                                                                   STATE: New York
                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 389 AAAGTCATTGTCGAGA 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAATCACTGTCAACA 368
                                                                                                                                                                              1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                      Sap, Jan M.
Ullrich, Ax
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                                                                                                                              U.S.A.
                                                                                                                                                                                                                                                                                                                                                                        Schlessinger, Joseph
                                                                                                                                                                                                       PENNIE & EDMONDS
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                     #1.25
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US-08-087-244A-3/c
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Best Local Similarity 45.5%;
Matches 115; Conservation
                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08087244A Patent No. 5863755
                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
TINFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
                   COMPUTER READABLE FORM:
                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                  TITLE OF INVENTION: NOVEL RECEPTOR-TY TITLE OF INVENTION: PHOSPHATASE-KAPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 212-790-9090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                STATE: New York
                                                                                           STREET:
                                  COUNTRY: U
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
MEDIUM TYPE: Floppy disk
                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4374 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3569
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Coruzzi, Laura A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAGAGGAGTTAGTCTGAGAGTCTATTCGAATCATATCAAATATGCAGCTTTAAATTCA 3510
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                                                                         New York
                                                                                                        1155 Avenue of the Americas
                                                                                                                                                                                                                       Vogel, Wolfgang
Fuchs, Miriam
                                                                                                                                                                                                                                                        Sap, Jan M.
Ullrich, Axel
                                                      U.S.A.
                                                                                                                                                                                                                                                                                                 Schlessinger, Joseph
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Pred. No. 1.3;
0; Mismatches 138;
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DB 2; Length 4374; Indels

0;

Gaps

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

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RESULT 15
US-09-440-325A-2/c
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                                                                                     SOFTWARE: FastSEQ for Windows
SEQ ID NO 2
LENGTH: 2082
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09440325A Patent No. 6280994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.3%;
Best Local Similarity 45.5%;
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/440,325A
CURRENT FILING DATE: 1999-11-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                 APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: Zacl: A Human Metalloenzyme
FILE REFERENCE: 98-79
    FEATURE:
OTHER INFORMATION: This degenerate sequence encodes the amino OTHER INFORMATION: sequence of SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4374 base pairs
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,244A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 212-790-9090
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 212-/90-907-707-1EFAX: 212-869-8864/9741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 01-JUL-1993 CLASSIFICATION: 435
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DEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGTAGCGTGTGC 341
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1..4371
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Pred. No. 1.3;
0; Mismatches 138;
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Search completed: July Job time: 43 secs
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                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                 7.2%;
Local Similarity 31.2%;
les 39; Conservation
                                                                   329 GCYTG 325
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                                                                                                                                     389 ARYTTNSWNARCATNCCRTTNACRTCNGGRTCYTTRAAYTGNGTNACYTTRAANARRTGN 330
                                                                                                                                                                                                      449 ARNARYTCRTTRTAYTCNCKNARYTCRTCYTTNSWNARNGCNGCYTTRTCDATRTTYTGN 390
                                                                                                                                                                   65 AGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCA 124
                                                                                                                                                                                                                                        5 AGGCTCTCGTTATTCTGGGGGTTTCTCTTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTG 64
                                                                                                                                                                                                                                                                          29;
                                                                                                                                                                                                                                                                                        Score 32;
Pred. No.
                                                                                                                                                                                                                                                                        Mismatches
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Minimum DB seq length: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
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                                                                          /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                        /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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36.8	36.8	38.9	38.9	38.9	38.9	38.9	41.8	41.8	41.8	42.8	56.3	59.7	60.3	60.3	60.3	62.8	100.0	100.0	Query Match
233	233	636	636	522	367	367	582	582	582	606	657	2467	478	478	478	748	10132	444	Query Match Length
10	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	10	10	10	DB
US-09-895-828-1	US-10-114-666-117	US-10-040-862-8226	US-09-796-692-8226	US-10-102-524-791	US-10-040-862-8055	US-09-796-692-8055	US-10-146-502-1606	US-09-878-178-1606	US-10-046-935-1606	US-10-060-036-2544	US-09-871-161-344	US-10-001-873-11	US-10-146-502-1085	US-09-878-178-1085	US-10-046-935-1085	us-09-969-347-31	US-09-978-199-3	US-09-978-199-1	ID ,
17	7	26	26	_	5	5	ğ	6	6	14	_		35	5	5	8			
Sequence 117, App	 Sequence 117, App 	Sequence 8226, Ap	Sequence 8226, Ap	Sequence 791, App	Sequence 8055, Ap	Sequence 8055, Ap	Sequence 1606, Ap	•	Sequence 1606, Ap	Sequence 2544, Ap	Sequence 344, App	Sequence 11, Appl	Sequence 1085, Ap	Sequence 1085, Ap	Sequence 1085, Ap	Sequence 318, App	Sequence 3, Appli	Sequence 1, Appli	Description

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APPLICANT: POGUE, GREGORY P.
APPLICANT: VELICHKO, SHARLENE
APPLICANT: VELIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 444; DB 10; Best Local Similarity 100.0%; Pred. No. 7.1e-134; Matches 444; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 60/240,967
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.1
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TYPE: DNA
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                                                                                                                                                                                                                                                                         121 GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT 180
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APPLICANT: POGUE, GREGORY P.
APPLICANT: VELICHKO, SHARLENE
TITLE OF INVENTION: PRODUCTION OF BOVINE LYSOZYME BY PLANT VIRAL VECTORS
FILE REFERENCE: 42202
CURRENT APPLICATION NUMBER: US/09/978,199
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 60/240,967
PRIOR APPLICATION NUMBER: 60/240,967
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN Ver. 2.1
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Best Local
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TYPE: DNA
ORGANISM: Bovine sp
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             TACGTTGAGGGTTGCACCCTGTAA 444
                                                                  CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT
                                                                                                                                            GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
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CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/60/237,598
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,604
PRIOR APPLICATION NUMBER: US/60/237,604
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 318
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 318
LENGTH: 748
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                                                                              Sequence 1085, Application Patent No. US20020156011A1 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Jiang, Yuqiu
APPLICANT: Harlocker, Susan
APPLICANT: Secrist, Heather
APPLICANT: Wang, Aijun
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                                                                                                                                                                                                                                       AGTTACGTTGAGGGTTGCACCCTGTAA 444
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Pred. No. 3.5e-80;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-046-935-1085
                                ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-878-178-1085
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CURRENT APPLICATION NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2239
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1085
LENGTH: 478
                                                                                                                                                                                                                                                                                                              Sequence 1085, Application US/09878178 Patent No. US20020177552A1 GENERAL INFORMATION:
                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1085
LENGTH: 478
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                                                                                                                                                                                                  APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/878,178
CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 2237
                                                                                                                                                                                                                                                                          APPLICANT: Jiang, Yuqiu APPLICANT: Harlocker, Susan L.
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Pred. No. 1:2e-76;
Score 267.8;
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US-10-146-502-1085
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APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527C2
CURRENT EPILLING DATE: 2002-05-14
CURRENT FILLING DATE: 2002-05-14
CURRENT FILLING DATE: 2002-05-14
CURRENT FILLING DATE: 2002-05-14
CURRENT SILLING DATE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1085
LENGTH: 478
TYPE: DNA
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137 GGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACTACAATCCTA 196
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                                                                                                   62 TGGCCAGAACTCTGAAAAGATTGGGAATGGATGGCTACAGGGGAATCAGCCTAGCAAACT
                                                                                                                                                                     77 TTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAGCCTGGCAAACT 136
                                                                                                                                                                                                                                                                        2 TTCTGGGGCTTGTCCTTTTCTGTTACGGTCCAGGGCAAGGTCTTTGAAAGGTGTGAGT 61
                                                                                                                                                                                                                                  2 TTCTGGGGCTTGTCCTCCTTTCTGTTACGGTCCAGGGCCAAGGTCTTTGAAAGGTGTGAGT 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGCCAGAACTCTGAAAAGATTGGGAATGGATGGCTACAGGGGAATCAGCCTAGCAAACT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATTAATGGAAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harlocker, Susan
Secrist, Heather
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78.0%;
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0; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 267.8; DB 9
Pred. No. 1.2e-76;
                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                        92;
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Sequence 11, Application US/10001873

Patent No. US20020160388A1

GENERAL INFORMATION:
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
APPLICANT: Turner; Leah

ITILE OF INVENTION: Compositions and Methods Rel
FILE REFERENCE: DEX-0275

CURRENT APPLICATION NUMBER: US/10/001,873

CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: 60/252,055

PRIOR APPLICATION NUMBER: 60/252,496

PRIOR APPLICATION NUMBER: 55

PRIOR FILING DATE: 2000-11-22

NUMBER OF SEQ ID NOS: 55

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SEQ ID NO 11
LENGTH: 2467
                                                                                                                                                                                                                                                                                                 Matches 345;
                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (2319)..(2319)
OTHER INFORMATION: a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                  Local Similarity
       180
                                     186 CTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTG
                                                                                            126 CCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAAGCTACAAA 185
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   GCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATTAATGGAAAATG
                                                                       CCTAGCAAACTGGATGTGTTTGGCCAAATGGGAGAGTGGTTACAACACACGAGCTACAAA
                                                                                                                                                                                                                       GGCTCTCATTGTTCTGGGGGCTTGTCCTCCTTTCTGTTACGGTCC-AGGCAAGGTCTTTGA
                                                                                                                                                                                                                                                      GGCTCTCGTTATTCTGGGGGTTTCTCTTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGA 65
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                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(657)
; OTHER INFORMATION: n = A,T,C
US-09-871-161-344
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CURRENT FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 09/328,111
PRIOR APPLICATION NUMBER: 60/217,393
PRIOR APPLICATION NUMBER: 60/217,393
PRIOR FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 60/098,639
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 344,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-260XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                               194 CTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTGGTGTAATG
                                                                                                                                                                                                                       134 ACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACTACAAATC 193
                 314 ATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTC----AGTGAGCAAGGCAT 368
                                                                                     254 ATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATTAATGGAAA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 AATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGA----GCA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 GTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 GTGTAATGATGGCAAAACCCCCAGGAGCAGTTAATGCCTGTCATTTATCCTGCAGTGCTTT
                                                                                                                                                                                                                                                                                            74 AGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGGACTCAGCCTGGCAA 133
                                                                                                                                                                                                                                                                                                                                               15 TTGTTCTGGGGCTTGTCCTCCTTTCTGTTACGGTCCAGGGCAAGGTCTTTGAAAGGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                       al Similarity 75.9
322; Conservative
                                                                                                                                                                                                                                                                                                                                                                    14 TTATTCTGGGGTTTCTCTTTCCTTTCTGTCGCTGTCCAAGGCCAAGGTCTTTGAGAGATGTG
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                                                     ATGGCAAAACCCCAGGAGCAGTTAATGCCTGTCATTTATCCTGCAGTGCTTTGCTGCAAG
                                                                                                                             CTGGAGACAGAAGCACTGATTATGGGATATTTCAGATCAATAGCCGCTACTGGTGTAATG
                                                                                                                                                                                                   ACTGGATGTGTTTGGCCAAATGGGAGAGTGGTTACAACACACGAGCTACAAACTACAATG 194
                                                                                                                                                                                                                                                                         AGTTGGCCAGAACTCTGAAAAGATTGGGAATGGATGGCTACAGGGGAATCAGCCTAGCAA 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTGCAAGATAACATCGCTGATGCTGGTAGCTTGTGCAAAGAGGGGTTGTCCGTGATCCACA 359
Application US/09871161 o. US20030097666A1
                                                                                                                                                                                                                                                                                                                                                                                                                                      56.3%;
75.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 250; DB 9; Length 657; Pred. No. 8.4e-71; 0; Mismatches 97; Indels
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RESULT 10
US-10-046-935-1606/c
; Sequence 1606, Application US/10046935
; Patent No. US20020156011A1
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APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, David H.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yuqiu
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TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036 |
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2544
LENGTH: 606
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   GENERAL INFORMATION:
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LOCATION: 603
OTHER INFORMATION: n = A,T,C or
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ORGANISM: Homo sapiens
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76.4%;
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APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF COLON CANCER
FILE REFERENCE: 210121.527
CURRENT APPLICATION NUMBER: US/09/878,178
CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 2237
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1606
LENGTH: 582
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                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-878-178-1606
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CURRENT FILING DATE: 2002-01-15
NUMBER OF SEO ID NOS: 2239
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1606
LENGTH: 582
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Best Local Similarity 76.5%;
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Best Local Similarity
                                                         Matches 241;
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APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527C1
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ORGANISM: Homo sapiens
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                                                      Score 185.4; DB 9;
Pred. No. 7.4e-50;
0; Mismatches 71;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-502-1606
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US-10-146-502-1606/c
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APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527C2
CURRENT APPLICATION NUMBER: US/10/146,502
CURRENT FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2241
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1606
LENGTH: 582
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APPLICANT: Harlocker, St
APPLICANT: Secrist, Heat
APPLICANT: Wang, Aijun
APPLICANT: Stolk, John P
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mes 241; Conserv
            430 GGTTGCACCCTGTAA 444
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                                                                               AGAGCATGGGTGGCATGGAGAAATCGTTGTCAAAACAGAGATGTCCGTCAGTATGTTCAA 283
                                                                                                        ACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGGTTACGTTGAG 429
                                                                                                                                                                             GATAACATCGCTGATGCTGGTAGCTTGTGCAAAGAGGGTTGTCCGTGATCCACAAGGCATT
                                                                                                                                                                                                                           AATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGA---GCAAGGCATT 369
                                                                                                                                                                                                                                                                         GATGGCAAAACCCCAGGAGCAGTTAATGCCTGTCATTTATCCTGCAGTGCTTTGCTGCAA 403
                                                                                                                                                                                                                                                                                                                                                                          GCTGGAGACAGAAGCACTGATTATGGGATATTTCAGATCAATAGCCGCTACTGGTGTAAT 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACTGGATGTGTTTGGCCAAATGGGAGAGTGGTTACAACACACGAGCTACAAACTACAAT 523
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76.5%;
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Pred. No. 7.4e-50;
0; Mismatches 71;
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US-09-796-692-8055
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PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-22
PRIOR FILING DATE: 2000-05-22
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LENGTH: 367
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Best Local Similarity
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
TITLE OF INVENTION: HEMAIOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
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NUMBER OF SEQ ID NOS: 9597
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PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
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LOCATION: (361)
OTHER INFORMATION: n=A,T,C
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                149 CCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACTACAATCCTAGCAGTGAAAGCA 208
                         329 CTGTAGCGTGTGCAAAGCATATTGTCAGTGA---GCAAGGCATTACAGCCTGGGTGGCAT
                                                                                                   269 ATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATTAATGGAAAATGACATCGCTAAAG 328
                                                                                                                                                                                                  209 CTGATTATGGGATATTTCAGATCAACAGCAAATGGTGGTGTAATGATGATGGCAAAACCCCCTA 268
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                                                                          GAGCAGTTAATGCCTGTCATTTATCCTGCAGTGCTTTGCTGCAAGATAACATCGCTGATG
                                                                                                                                                                     CTGATTATGGGATATTTCAGATCAATAGCCGCTACTGGTGTAATGATGGCAAAACCCCAG 120
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Conservative
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LENGTH: 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILLING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILLING DATE: 2000-03-17
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TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
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CURRENT FILING DATE: 2001-11-06
                                                                                                                                                                                                                                        NAME/KEY: unsure LOCATION: (361) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure LOCATION: (331) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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                                                                                                                                    Local Similarity es 227; Conserv
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FILING DATE: 2000-04-27
APPLICATION NUMBER: US 60/200,303
FILING DATE: 2000-04-28
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APPLICATION NUMBER: US 60/223,378
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209 CTGATTATGGGATATTTCAGATCAACAGCAAATGGTGGTGTAATGATGGCAAAACCCCCTA 268
                                                                  149 CCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACTACAATCCTAGCAGTGAAAGCA 208
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                                         CCAAATGGGAGAGTGGTTACAACACACGAGCTACAAACTACAATGCTGGAGACAGAAGCA
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Corixa Corporation
                                                                                                                                    Conservative
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Pred. No. 8.1e-46;
0; Mismatches 69
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SEQ ID NO 791
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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CURRENT FILING DATE: 2002-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mannion, Jane
APPLICANT: Gaiger, Alexander
APPLICANT: Gordon, Brian
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERASTIONS DIAGNOSIS OF KIDNEY CANCER
FILE REFERENCE: 210121.572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 447, 456, 466
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 522
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                           386 GGAAAAGTCATTGICGAGACCATGACGTCAGCAGTTACGTTGAGGGTTGCACCCTGTAA 444
                                                                                                                                                         181 CTGTAGCTTGTGCAAAGAGGGTTGTCCGTGATCCACAAGGCATTAGAGCATGGGTGGCAT 240
                                                                                                                                                                                                   269 ATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATTAATGGAAAATGACATCGCTAAAG
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                                                                                                                                                                                                                                                                                                                                                               149 CCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACTACAATCCTAGCAGTGAAAGCA 208
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SOURCE SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES	RESULT 1 108277 LOCUS DEFINITION ACCESSION VERSION VERSION		44 45	436	4 1	40	38	35 37	. ω (ພຸພ ພ 4	32	30 31	29	27 28	26	2 2 5 4	23	21	20	1 18 8	17	15	14	1 2	11	19	æ ~	1 O	4. D	- ω	22 12	Result No.
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FEATURES	JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	108277	RESULT 1
Location/Qualifiers	Patent: EP 0374913-A1 2 27-JUN-1990;	Pichia pastoris glyceraldehyde-3-phosphate dehydrogenase gene	Digan, M.E.	1 (bases 1 to 459)	Unclassified.	Unknown.	Unknown.	•	I08277.1 GI:589012	108277	Sequence 2 from Patent EP 0374913.	I08277 459 bp DNA		
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translation="MKALVILGFLFLSVAVQGKVFERCELARTLKKLGLDGYKGVSLA"
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Pred. No. 6.4e-249;
                                                                                                                                                                                and the evolution of bovine
                                                                                                                                                          11387-11393 (1989)
                                                                                                                                                                                                                                                                                                       951 bp
e 2b mRNA,
                                                                                                                                                                                                                                                            mRNA, clone lambda-cBL[12,42]
                                            2b precursor"
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                                                                                                                        [1] kindly submitted
                                                                                                                                                                                                                           Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                444;
                                                                                                                                                           Takeuchi,K., Irwin,D.M., Gallup,M., Shinbrot,E., Ka Stewart,C.B. and Basbaum,C. Multiple cDNA sequences of bovine tracheal lysozyme J. Biol. Chem. 268 (36), 27440-27446 (1993) 94086565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 138
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                                                                                                                                            8262986
                                                                                                                                                                                                                                                 Bovidae; Bovinae; Bo
1 (bases 1 to 1060)
                                                                                                                                                                                                                                                                                                                      Bos taurus
                                                                                                                                                                                                                                                                                                                                     Bos taurus (cow).
                                                                                                                                                                                                                                                                                                                                                         lysozyme.
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                               /organism="Bos taurus"
/db_xref="taxon:9913"
/cell_type="epithelial/
/tissue_type="trachea"
                  /dev_stage="adult"
                                                                                                                        Location/Qualifiers
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73. .459
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Mirkov, T.Erik. and Fitzmaurice, L.C.
Protection of plants against plant
Patent: US 5422108-A 1 06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                          Unclassified.
                                                                                                                                                                                                                                                                                                                                                                        Unknown
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                                            GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG 143
                                                                         GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG 125
                                                                                                      GGCTCTCGTTATTCTGGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGA
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68 GATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAGCC
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M26241 J04831 M27181
M26241.1 GI:163314
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Irwin, D.M. and Wilson, A.C.
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                                             CTCTCGTTATTCTGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGAGA 62
                                                             CTCTCGTTATTCTGGGGTTTCTCTTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGAGA 67
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                                                                                                      Conservative
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                                                                                                                                                                                                         /note="lysozyme 2a signal peptide" 50...436
                                                                                                                                                                            /product="lysozyme
154 c 187 g
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                                                                                                                                                                                                                                                                  /protein_id="aaa30628.1"
/db_xref="GI:163315"
/translation="TLVILGFLFLSVAVQGKVFERCELARTLKKLGLDGYKGVSLANW
LCLTKWESSYNTKATNYNPSSESTDYGIFQINSKWWCNDGKTPNAVDGCHVSCSELME
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                                                                                                                                                                                                                                                                                                                                        /note="lysozyme 2a precursor"
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                                                                                                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
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                                                                                                                                                                                                                                                                                                                                                                                                                 Patent:
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  GATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAGCC
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                                                          ACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTGGT
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llarity 100.0%; Pred. No. 8.2e-245;
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                                                                                                                                                                   Draft entry and computer-readable sequence by D.M.Irwin, 23-JUN-1989.
Location/Qualifiers
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89291894
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Bovidae; Bovinae; Bos.
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Irwin,D.M. and Wilson,A.C.
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                                                                                                             GCTATAAGGGAGTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGTTACGTTG
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                                                                                                                                                                                                                                                                                              285
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                                                                                                                                                                                                                                                                                                                          /note="lysozyme 2c signal peptide"
10. .396
                                                                                                                                                                                                                                                                                                                                                               /translation="vkgkvfercelartlkklgldgykgvslanwlcltkwessyntk
ATNYNPSSESTDYGIFQINSKWWCNDGKTPNAVDGCHVSCSELMENDIAKAVACAKHI
VSEQGITAWVAWKSHCRDHDVSSYVEGCTL"
                                                                                                                                                                                                                                                                                              /product="lysozyme 2c"
142 c 181 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAA30630.1"
/db_xref="GI:163319"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="lysozyme 2c precursor"
                                                                                                                                                                                                                        89.0%; Score 395; DB 4; Lo
100.0%; Pred. No. 3.8e-220;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                            181 g
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Best Local Similarity
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                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae; Bovinae; Bos.
1 (bases 1 to 786)
Irwin,D.M. and Wilson,A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multiple cDNA sequences and the evolution of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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M26240 J04831 M27184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATCCTGCAGCGAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACGTCAGCAGTTACGTTGAGGGTTGCACCCTGTAA 399
           CTGGGTGGCATGGAAAAGTCATTGTCGAGACCCATGACGTCAGCAGTTACGTTGAGGGTTG
                                                                          TGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAGCAAGGCATTACAGC
                                                                                                        TGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAGCAAGGCATTACAGC
                                                                                                                                                                        TGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATTAATGGAAAA 314
                                                                                                                                                                                                       TAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTGGTGTAATGA 126
                                                                                                                                                                                                                                                                       CTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACTACAATCC
                                                                                                                                                                                                                                                                                    CTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACTACAATCC 194
                                                                                                                                      TGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATTAATGGAAAA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B101
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                                                                                                                                                                                                                                                                                                                                                                                                                    256
                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id-"AAA30631.1"|
/db_xref-"G1:163321"
/translation-"ASWICCLIKWEŚSYNTKATNYNPSSESTDYGIFQINSKWWCNDGK
TPNAVDGCHVSCSELMENDIAKAVĄCAKHIVSEQGITAWVAWKSHCRDHDVSSYVEGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Bos taurus"
/db_xref="taxon:9913"
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||||||||||
307 CACCCTGTAA 316
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                                                                                                                                          202
                                                                                                                                                           194 CTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTGGTGTAATG
                                                                           262
                                                                                                                                                                                                                                        134 ACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACTACAATC
                                                                                                           254 ATGGCAAAACCCC 266
                                                                                                                                                                                                                                                                                                                                                                                                       252;
                                                                                                                                                                                                                                                                                      74 AGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAGCCTGGCAA 133
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Bovine lysozyme c isozyme 3a mRNA, complete cds.
M26242 J04831 M27180
M26242.1 GI:163322
                                                                                                                                                                                                                                                                                                                                     22 TTATTCTGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGAGAGATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Draft entry and computer-readable sequence for by D.M.Irwin, 23-JUN-1989.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 264 (19), 11387-11393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Multiple cDNA sequences and the evolution of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 1082)
Irwin, D.M. and Wilson, A.C.
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BOVLYSOZMB
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                                                                                                                                          CTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTGGTGTAATG
                                                                                                                                                                                                        AGCTTGCCAGAACTCTGAAGAAACTTGGACTGGATGGCTATAAGGGAGTCAGCCTGGCAA
                                                                                                                                                                                                                                                                                                                                                        TTATTCTGGGGTTTCTCTTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGAGAGATGTG
                                                                             ATGGCAAAACCCC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="lysozyme 3a signal peptide"
63. .449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAA30632.1"
/db_xref="GI:163323"
/translation="MKALILIGELFLSVAVQGKVFERCELARTLKKLGLDGYKGVSLA
/walcltkwessyntkatnynpssestdygifqinskwwcndgktpnavdgchvscsel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="lysozyme 3a"
205 c 209 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9913"
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99.6%;
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Pred. No. 7.8e-107;
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BASE COUNT
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ORGANISM
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Irwin,D.M., White,R.T. and Wilson,A.C.
Characterization of the cow stomach lysozyme genes: repetitive DNA
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        3031
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Evol. 37 (4), 355-366 (1993)
                                                                     /label=exon3
7575..8130
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                    /label=exon4
                                                    /note="putative"
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/note="putative"
/rpt_family="BCS"
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4381. .4510
                                                                                                                                                                                                                                                                                                                                                             4113. 4238
/gene="1ysozyme"
/note="putative"
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NWLCLTKWESSYNTKATNYNPSSESTDYGIFGINSKWWCNDGKTPNAVDGCHVSCSEL
MENDIAKAVACAKHIVSEQGITAWVAWKSHCRDHDVSSYVEGCTL"
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/rpt_family="Nla"
                                                                                                                                     'note="putative"
                                                                                                                                                                                                                                     'gene="lysozyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=exon1
join(2537. .2672,3840. .4004,6136. .6211,7575. .7641)
/gene="lysozyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                 'label=exon2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="putative"
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. .8130
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     1909 g
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BOVLYSOZMC
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MEDLINE
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1 (bases 1 to 8051)

Irwin,D.M., White,R.T. and Wilson,A.C.

Characterization of the cow stomach lysozyme genes: repetitive DNA
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                                                                                                                 3645.
                                                                                                                                                                                                              /translation="mKaliilgflflsVavQGKvfERCELARTLKKLGLDGYKGVSLA
NWLCLTKWESSYNTKATNYNPSSESTDYGIFQINSKWWCNDGKTPNAVDGCHVSCSEL
MENDIAKAVACAKHIVSEQGITAWVAWKSHCRDHDVSSYVQGCTL"
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/note="putative"
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                'gene="lysozyme"
                                                            /note="putative"
/rpt_family="Bovine Concensus Sequence (BCS)"
                                                                                              /gene="lysozyme"
                                                                                                                                                                                                                                                                                                                               /gene="lysozyme"
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                                                                                                                                                                                                                                                                                                                                                                                          /gene="lysozyme"
/note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                              716. .904
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="lysozyme"
join(716. .904,2158. .2322,4118. .4193,7192. .7755)
                                                                                                                                                                                                                                                                                                              /codon_start=1
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/db_xref="taxon:9913"
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                                                                                                                                label=exon2
                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene=
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                                               t_type=dispersed
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                                   .4193
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VERSION
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                                                                                                                                                                                                                                                                                                             JOURNAL
MEDLINE
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TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 881)
Irwin,D.M. and Wilson,A.C.
Concerted evolution of ruminant stomach lysozymes.
of lysozyme cDNA clones from sheep and deer
J. Biol. Chem. 265 (9), 4944-4952 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHPLZMIB 881 bp
Sheep lysozyme ib (lzmib) mRNA,
M32493 J05279
M32493.1 GI:165965
Lysozyme ib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sheep abomasum, cDNA to mRNA. Ovis aries
                                                                                                                                                                                                                                                         Draft entry and computer-readable by D.M.Irwin, 01-MAR-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Caprinae; Ovis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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/product="lysozyme 1b"
1. .17
                                                                                                                                                                                   /organism="Ovis aries"
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1453 c
                                                                                                                                        /codon_start=
                                                                                                                                                     'note="lysozyme 1b precursor"
                                                                                                                                                                                                                                         location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'rpt_family="BCS dimer"
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2. .7755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3' mRNA
                                                                                                                                                                                                                                                                        sequence for [1] kindly submitted
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AUTHORS
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ORGANISM
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SHPLZM1C
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 LOCUS
                              RESULT 14
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VERSION
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ORIGIN
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MEDLINE
PUBMED
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Best Local :
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                                                                                                                                                                   100 GGACTGGACGGCTATAAGGGAGTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAA 159
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                                                                                                        160 AGCAGTTATAACACAAAAGCTACAAACTACAATCCT 195
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                                                                                                                                       46 GGACTGGACGGCTATAAGGGAGTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAA 105
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1 (bases 1 to 881)
Irwin,D.M. and Wilson,A.C.
Concerted evolution of ruminant stomach lysozymes.
of lysozyme cDNA clones from sheep and deer
J. Biol. Chem. 265 (9), 4944-4952 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sheep lysozyme 1c (lyz1c) mRNA,
M32494 J05279
M32494.1 GI:165967
 SHPLZM2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Draft entry and computer-readable sequence for by D.M.Irwin, 01-MAR-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90202968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sheep abomasum, cDNA to mRNA
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                                                                                                                                                                                                                                                                                285
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                                                                                                                                                                                                                                                                               /note="PCR primer"
144 c 183 g
                                                                                                                                                                                                                                                                                                               /product="lysozyme 1c"
1. .17
                                                                                                                                                                                                                                                                                                                                                         QGITAWVAWKSHCRDHDVSSYVEGCSL"
                                                                                                                                                                                                                                                                                                                                                                      /translation="KVFERCELARTLKELGLDGYKGVSLANWLCLTKWESSYNTKATNYPGSESTDYGIFQINSKWWCNDGKTPNAVDGCHVSCSELMENNIAKAVACAKHIVSE
                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAA31559.1"
/db_xref="GI:165968"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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145 c 182 g
                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="lysozyme lc precursor"
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100.0%; Pred. No. 1.3e-44;
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Pred. No. 1.3e-44;
                                                                                                                                                                                                                                                                             183 g
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881 bp
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                                                                                                                                                                                                                                                                                269 t
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mRNA
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MAM 27-APR-1993
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DEFINITION
ACCESSION
VERSION
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BOVLSZ1B
LOCUS
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AUTHORS
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MEDLINE
PUBMED
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MEDLINE
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    source
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les 96; Conserv
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                                                                                                                                                                                                                                                                                                                         891 bp
Bovine lysozyme c isozyme 1b mRNA,
M26246 J04831 M27179
M26246.1 GI:163312
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea

Bovidae; Caprinae; Ovis.

1 (bases 1 to 881)

Irwin,D.M. and Wilson,A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Concerted evolution of ruminant stomach lysozymes. Characterization of lysozyme cDNA clones from sheep and deer J. Blol. Chem. 265 (9), 4944-4952 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sheep lysozyme 2a (lyz2a) mRNA, M32495 J05279
                                    Draft entry and computer-readable sequence for [1] kindly submitted by D.M.Irwin, 23-JUN-1989.
                                                                                                                                                        Multiple cDNA sequences and the evolution of bovine
                                                                                                                                                                           1 (bases 1 to 891)
Irwin, D.M. and Wilson, A.C.
                                                                                                                                                                                                                 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                           Bovine abomasum, cDNA to mRNA, clones lambda-cBL[3,4,35]. Bos taurus
                                                                                                                                                                                                                                                                                                                 lysozyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Draft entry and computer-readable sequence by D.M.Irwin, 01-MAR-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sheep abomasum, cDNA to mRNA.
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lysozyme 2a.
                                                                                                   89291894
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                                                                                                                                      lysozyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGACTGGACGGCTATAAGGGAGTCAGCCTGGCAAACTGGTTGTGTTTTGACCAAATGGGAA 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.6%; Score 96; DB 4; Interest 100.0%; Pred. No. 1.3e-44; Conservative 0; Mismatches 0;
                                                                                                                  . Chem. 264 (19), 11387-11393 (1989)
Location/Qualifiers
1. .891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAA31560.1"
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/translation="Kverercellartlkelgldgykgvslanwiclitkwessyntkatn
/translation="Kverercellartl"
NGGITAWVAWKSHCRDHDVSSYVEGCTL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="PCR primer"
144 c 183 g
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/db_xref="taxon:9940"
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                                                                                                                                                                                                                                                                                                                                                                        mRNA linea complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                      Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                               MAM 27-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Job time
               Search completed: July
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: 1382 secs
                                                              81
                                                                                           74 AGCTTGCCAGAACTCTGAAGAAACTTGGACTGGA 107
                                                                                                                             21 TTATTCTGGGGTTTCTCTTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGAGAGATGTG
                                                                                                                                          14 TTATTCTGGGGTTTCTCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGAGAGATGTG 73
                                                                                                                                                                                                            Similarity
                                                              274
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                           þ
                                                                                                                                                                                                                                                                                                                                                    /proteIn_1d="AAA30627.1"
/db_xref="GI:163313"
/db_xref="GI:163313"
/translation="MKALILIGELELSVAVQGKVFERCELARTLKKLGLDGYKGVSLA
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MENEIAKAVACAKQIVSEQGITAWVAWKSHCRDHDVSSYVEGCTL"
                                                                                                                                                                                                                                                                                                        /note="lysozyme 1b signal peptide" 62. 448
                                                                                                                                                                                                                                                                        /product="lysozyme lb" 152 c 196 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="lysozyme 1b precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Bos taurus'
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                                                                                                                                                                                                         21.2%;
                2003, 07:02:34
                                                                                                                                                                                           0;
                                                                                                                                                                                                           Score 94; DB 4;
Pred. No. 2e-43;
                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                           269 t
                                                                                                                                                                                             0;
                                                                                                                                                                                                                          Length 891;
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OLIGO_NUC
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AAL19009	ABL22715	AAH94220	AAX05828	ABL62119	AAS18958	AAI96554	AAS84866	AAK62628	ABV37238	×		AAD32015	AAQ37838	AAS52837	AAK82227	AAF55437	ABK16005	AAI28977	AAF28652	AAQ03368	AAD39104	AAS66076	ABV24794	AAS65881	AAD17725	AAN92386	AAQ03369	ABK64517	ABL70110	ABQ58989	AAA16339	ABL38017	AAN70949	ABL37496	AAN70943
Human breast cance	Drosophila melanog	Human foetal cDNA,	Human pheromone re	Colon adenocarcino	Human cadherin-lik	Human neuroblastom	DNA encoding novel		Human prostate exp	Sequence of the PC	Methanococcus jann		Sequence of the co	Enterococcus faeca	Human immune/haema	Nucleotide sequenc	Human lung tumour	Colon tumour relat		Sequence of human	Human lung-specifi	DNA encoding novel	Human prostate exp	DNA encoding novel	Human macrophage-e	DNA coding for the	Sequence encoding	Human benign prost	eas can	colon	colon		Sequence encoding	O	Sequence encoding

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ALIGNMENTS

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RESULT 1
AAD39128
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XX AAD39128
AC AAD3
XX BOV1
DT 04-C

Pogue G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD39128 standard; DNA; 444 BP.
                                                                                                                                                                                                                                                                                               17-OCT-2001; 2001WO-US32147
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          Velichko
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/product= "Bovine lysozyme"
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Result No.

Score

Query Match

Length DB

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Description

SUMMARIES

100.0 100.0 100.0 98.9 98.4 75.9 6.8 6.8

459 10130 964 964 964 390 435

24 24 20 10 14 10 22

AAN92054 AAD17740

> Sequence encoding Sequence of human

Human macrophage-e

ss sequence of cDN Bovine lysozyme c

AAD39128 AAQ05054 AAD39129 AAV08922 AAN92057 AAQ39092 AAN70944

> Bovine lysozyme DN Sequence encoding p1044-BoLys plasmi Bovine Lysozyme c2

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RESULT 2
AAQ05054
ID AAQ0
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic plants that express heterologous DNA that encode a ruminant lysozyme, preferably bovine. This lysozyme protects against diseases caused by plant pathogens particularly bacterial pathogens. The method is useful for producing bovine lysozyme in host plants e.g. grapevines. Plasmid encoding a recombinant plant virus which comprises a bovine lysozyme encoding nucleic acid, is useful for producing bovine lysozyme in a plant. It is also useful for producing bovine lysozyme for an anti-xylella reagent for development of a recombinant source of Bolys protein for treating grapevines against pierce's disease (PD). The method is useful for protecting grapevines against xylella fastidiosa bacterium infection that causes PD. The present sequence is bovine lysozyme DNA.
              Sequence encoding bovine lysosyme c2
                                              30-OCT-1990
                                                                                                       AAQ05054 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Producing bovine lysozyme (BoLys) in plants e.g. grapevines, useful for protecting grapevines against Pierce's disease by infecting host plant with recombinant virus containing nucleic acid encoding BoLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 444 BP; 128 A; 86 C; 117 G; 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAAGGCTCTCGTTATTCTGGGGTTTCTCTTTCTTTCTGTCGCTGTCCAAGGCAAGGTC
                                            (first entry)
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                                                                                                        DNA;
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Pred. No. 1.2e-222;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAPDH locus without disrupting the g
the cell to produce bovine lysosyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence may be inserted into the DNA of Pichia pastoris at the GAPDH locus without disrupting the gene activity, transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 10; Table 2; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel DNA fragments comprising Pishia pastoris GAPDH gene it's 5'-regulatory region and 3'-transcription termination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PHIP ) PHILLIPS PETROLEUM CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-DEC-1988;
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            TACGTTGAGGGTTGCACCCTGTAA 444
                                                           CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGAGCCATGACGTCAGCAGT
                                                                                                       GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                                                                                                                           TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTTGGACTGGACGGCTATAAGGGA 120
                                                                                             GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                                                                                                                                                                                         ACAAACTACAATCCTAGCAGTGAAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                                                                                                                                                                                                           TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA
                                                                                                                                                                                                                                                                                                                                                       ATGAAGCTCTCGTTATTCTGGGGTTTCTCTCTTTCTGTCGTCGCTGTCCAAGGCAAGGTC
TACGTTGAGGGTTGCACCCTGTAA
                                              CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT
                                                                                                                                                                                              ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                                                                                                                                                                                                                                   GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT 180
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88US-0289357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89EP-0123652
                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                  Score 444; DB 11;
Pred. No. 1.2e-222;
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Length
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RESULT 3
AAD39129
ID AAD3
XX
AC AAD3

AAD39129

standard; DNA; 10130

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Matches
                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                     The invention relates to viral vectors and methods for producing transgenic plants that express heterologous DNA that encode a ruminant lysozyme, preferably bovine. This lysozyme protects against diseases caused by plant pathogens particularly bacterial pathogens. The method is useful for producing bovine lysozyme in host plants e.g. grapevines. Plasmid encoding a recombinant plant virus which comprises a bovine lysozyme encoding nucleic acid, is useful for producing bovine lysozyme pencoding nucleic acid, is useful for producing bovine lysozyme in a plant. It is also useful for producing bovine lysozyme recombinant source of BoLys protein for treating grapevines against sierce's disease (PD). The method is useful for protecting grapevines against xylella fastidiosa bacterium infection that causes PD. The present sequence is p1044-BoLys plasmid DNA containing bovine lysozyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric - Bos sp.
Chimeric - Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Producing bovine lysozyme (BoLys) in plants e.g. grapevines, useful for protecting grapevines against Pierce's disease by infecting host plant with recombinant virus containing nucleic acid encoding BoLys .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-479667/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-Xylella reagent; grapevine; cyclic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovine; viral vector; transgenic plant; lysozyme; antibacterial; Pierce's disease; PD; Xylella fastidiosa bacterium infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pl044-BoLys plasmid DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-OCT-2001; 2001WO-US32147
                                                                                                                                                                                                                                                                                                                              Sequence 10130 BP; 2854 A; 2078 C; 2492 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-OCT-2000; 2000US-240967P
                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                              5767
5947
                                                              5887
                                181
                                                                                               121
                                                                                                                                                                                                                                                             444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Fig 2; 36pp; English.
                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LARGE SCALE BIOLOGY CORP
               ACAAACTACAATCCTAGCAGTGAAAGCACTGÄTTATGGGATATTTCAGATCAACAGCAAA
                                                                               GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT
                                                                                                                               TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA
                                                                                                                                                TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120
                                                                                                                                                                                              ATGAAGGCTCTCGTTATTCTGGGGTTTCTCTTCTTTCTGTCGCTGTCCAAGGCAAGGTC
ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                              GTCAGCCTGGCAAACTGGTTGTGTTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT
                                                                                                                                                                                                                             ATGAAGGCTCTCGTTATTCTGGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Velichko S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Bovine lysozyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                           Score 444; DB 24;
Pred. No. 1.2e-222;
                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
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                                                                                                                                                                                                                                                                                                                              2706 T;
                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                          Length 10130;
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6006
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                                                                                                                               5886
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RESULT 4
AAV08922
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밁
                                                                                                                                                                                                                                              12-JAN-1995;
19-SEP-1991;
25-NOV-1991;
22-APR-1997;
                  This sequence encodes the bovine lysozyme c2 and can be used in the transgenic plant of the invention. The transgenic plant is resistant to plant pathogens and contains heterologous DNA encoding a ruminant or ruminant-like lysozyme, the plant expresses sufficient levels of the lysozyme to render it less susceptible to the pathogens than the wild-type plant. The plants are resistant to bacterial pathogens such as Pseudomonas syringae or Erwinia carotovora.
                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                   Bos sp
                                                                                                                                                                                                                                                                                                                                                                                                                                          pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine Lysozyme c2 protein coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV08922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV08922 standard;
                                                                                                                                Transgenic plants resistant to bacterial ruminant lysozyme gene
                                                                                                                                                                    P-PSDB;
                                                                                                                                                                               WPI; 1999-069855/06
                                                                                                                                                                                                     Fitzmaurice LC,
                                                                                                                                                                                                                                                                                                       22-APR-1997;
                                                                                                                                                                                                                                                                                                                             15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                   US5850025-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lysozyme;
                                                                                                            Example 1;
                                                                                                                                                                                                                         (SIBI-) SIBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6187 TACGTTGAGGGTTGCACCCTGTAA 6210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421
                                                                                                                                                                     AAW73502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGAGACCATGACGTCAGCAGT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                           resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACGTTGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                    signal peptide;
                                                                                                              Column 37-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                            NEUROSCIENCES
                                                                                                                                                                                                                                                91US-0762679.
91US-0798223.
97US-0919093.
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                                                                                                                                                                                                                                                                                                       97us-0919093
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
25..462
/*tag= a
                                                                                                                                                                                                     Mirkov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA;
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                                                                                                            23pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic plant;
                                                                                                                                                                                                                             INC
                                                                                                              English.
                                                                                                                                               pathogens -
                                                                                                                                                                                                                                                                                                                                                                                                                                                     plant pathogen;
                                                                                                                                              contain
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Matches 439; Best Local Similarity

Conservative

0,

Mismatches

Query Match

98.9%; 100.0%;

Score 439; Pred. No.

4.9e-220; DB 20;

Length 964; Indels

0,:

Gaps

0

Sequence 964 BP; 297

A; 165 C; 201 G; 301 T;

0 other;

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  (SALK ) SALK
                    02-NOV-1987;
                                                      18-MAY-1989
                                                                                                                mat_peptide
                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                      ss sequence
lysozyme C2
                                                                       WO8904320-A
                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                            Bovine
                                                                                                                                                                                                                                   Bovine lysozyme C2; protein signal sequence; Pinchia
                                                                                                                                                                                                                                                                               07-APR-1990
                                                                                                                                                                                                                                                                                                               AAN92057 standard; DNA; 964
                                                                                                                                                                                                                                                                                                                                                           444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCTCTCGTTATTCTGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGA
                                                                                                                                                                                                                                                                                                                                                         TGAGGGTTGCACCCTGTAA 462
                                                                                                                                                                                                                                                                                                                                                                 TGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                                                                                                                                                                                         CATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGTTACGT
                                                                                                                                                                                                                                                                                                                                                                                                  CATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGTTACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACACAAAAGCTACAAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTG
                                                                                                                                                                                                                                                   of cDNA insert of clone lambda BL3 encoding together with 3' untranslated region.
  INST FOR BIOL STUD
                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                              (first entry)
                   87US-0115940.
                                    88WO-U503907
                                                                                             /*tag= c
463..964
                                                                                                      /*tag= c
68..462
/*tag= d
                                                                                                                               /standard_name=
25..462
                                                                                                                                                        /standard_name=
942..964
                                                                                                                                                                                           Location/Qualifiers
                                                                                       /*tag=
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                                                                                                                                       "EcoRI Adaptor
                                                                                                                                                                "EcoRI Adaptor"
                                                                                                                                                                                                                                   pastoris
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RESULT 6
AAQ39092
ID AAQ3
XX
AC AAQ3
XY
DT 20-J
XX
BOV1
XX
BOV1
XX
KW BOV1
KW Gram
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KW Gram
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
       Bovine; lysozyme c; transgenic; plant; resistance; pathogen; gram negative; bacteria; hen egg white lysozyme; potato; tobacc tomato; carrot; apple; sunflower; petunia; violet; Pseudomonas; Agrobacterium; Xanthomonas; Erwinia; Clavibacter; ss.
                                                 Bovine lysozyme c DNA.
                                                                    20-JUL-1993
                                                                                                     AAQ39092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1989-165613/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Digan ME, I
Williams ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                               446
                                                                                                                                                                                                                  326
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                    standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                    DNA;
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The 3'-noncoding sequence does not contain a polyadenylation signal or a poly (A)+ tail. The 5'-terminus does not contain the ATG triplet corresponding to the translation initiation codon fo the pre-lysozyme C2 mRNA. Thus the cDNA insert encodes 16 amino acids amino-terminal to the amino-terminus of the mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prodn. of animal lysozyme - consists of P. pastoris for transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 964 BP; 298 A; 165 C; 200 G; 301 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pages 26-29; ; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 TGGCAAACTGGTTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 GATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAGCC
                                                                                                                                                                                                                                                                                                                                                        TGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAGCAAGGCA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCTCGTTATTCTGGGGTTTCTCTTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGAGA
                                                                                                                                                                                           AGGGTTGCACCCTGTAA
                                                                                                                                                                                                                 AGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                                                                        GTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTGGT
                                                                                                                                                                                                                                                                                                                   TTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGTTACGTTG 427
                                                                                                                                                                                                                                                                                                                                                                                                                                           GTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAGCC 127
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.4%; Score 437;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C from pichia pastoris by secretion promoter and terminator DNA
                                                                                                                                                                                           462
                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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5.5e-219;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Siegel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protect plants such as potatoes, tobacco, tomatos, carrots, apples, sunflowers, petunias and violets from plant pathogens such as Pseudomonas, Agrobacterium, Xanthomonas, Erwinia and Clavibacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence encodes bovine lysozyme c. This sequence was used in the production of transgenic plants that are resistant to pathogens. The lysozyme encoded by this sequence has a greater ability to lyse gram negative bacteria than hen egg white lysozyme and also has a greater stability. The lysozyme may be applied directly to treat or protect plants such as notations to there or to the contract analyse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protection of plants against plant pathogens - by transforma with DNA encoding a ruminant or ruminantilike lysozyme, esp. bovine lysozyme C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAR34010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-117142/14.
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25-NOV-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 73-74; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMAR-) SMART PLANTS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-SEP-1992;
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al Similarity 99.58;
437; Conservation
              426
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                                                                                                                                                                                                                                                                                                                                                                     TGAGGGTTGCACCCTGTAA 444
                                       CATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGTTACGT 425
                                                                                                         AATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAGCAAGG
                                                                                                                                                               GTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATT
                                                                                                                                                                                                     CTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTG
                                                                                                                                                                                                                     CTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTG
                                                                                                                                                                                                                                                            CGTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAA
                                                                                                                                                                                                                                                                        CCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAAGCTACAAA 185
                                                                                                                                                                                                                                                                                                                GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGCGAGTCAG
                                                                                                                                                                                                                                                                                                                                 GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG 125
                                                                                                                                                                                                                                                                                                                                                                                               GGCTCTCGTTATTCTGGGGTTTCTCTTTCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                964 BP;
                                                                                                                                                 GTGTAATGATGGCAAAACCCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATT
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91US-0798223
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25..459
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 A; 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mirkov TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; 201 G; 301 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 337; DB 14;
Pred. No. 1:5e-166;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 964;
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AAN92054
ID AANN
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KW Plas
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                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                     A cDNA bank was constructed using total RNA isolated from the human lymphoma cell line U-937. The bank was tested by hybridising with two radio-labeled 17-mer oligonucleotides (equiv. to the AA sequences 26-31 and 63-68 of HLZ). Clones isolated were designated pHL 14-1; pHL21 and pHL 23 (contg. an approx. 500 bp insert) and pHL2 and pHL8 (contg. a 300 bp insert).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New hybrid plasmids contg. sequences for human e\cdot g, as antiviral and antibacterial agent, and
                           Plasmid pHLZ100; human placental pre-lysozyme C; human milk lysozyme; human histiocytic lymphoma cell line U-937 pre-lysozyme C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; p2; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1987-136923/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sledziewski A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-NOV-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence encoding mature human lypozyme (HLZ).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAN70944;
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                                                                                             07-APR-1990
                                                                                                                       AAN92054;
                                                                                                                                                                                                                                                                                                                             Sequence 390 BP; 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BOEH ) BOEHRINGER INGELHEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-NOV-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAY-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibacterial;
                                                                Sequence of human pre-lysozyme C of placental origin.
                                                                                                                                                 AAN92054 standard; DNA; 435
                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                    150 AAGCACTGATTATGGGATATTTCAGATCAA 179
                                                                                                                                                                                                                                  204 AAGCACTGATTATGGGATATTTCAGATCAA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            444 TGAGGGTTGCACCCTGTAA 462
                                                                                                                                                                                                                                                                        30;
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85DE-3540075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlebowicz-Sledziewska E ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                   6.8%; 5c.
100.0%; Pr
                                                                                                                                                                                                                                                                                                                             A; 68 C; 113 G; 96
                                                                                                                                                                                                                                                                       Score 30; DB;; Pred. No. 1.6; 0; Mismatches
                                                                                                                                                 ВP
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                                                                                                                                                                                                                                                                                     DB 8; L
                                                                                                                                                                                                                                                                                                                              T; 0 other;
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                                                                                                                                                                                                                                                                                                  Length 390
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    useful
    d hosts.

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RESULT 9
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Best Local Similarity
                                             Human; macrophage-expressed protein; inflammation; angiogenesis; cancer; transplantation; myelodysplastic syndrome; transgenic animal; ischaemia; gene therapy; Crohn's disease; immune disorder; myeloid leukaemia; shock; sepsis; nephritis; genetic disorder; nervous system disease; neuropathy; Alzheimer's disease; parkinson's disease; multington's disease; fibrosis; amyotrophic lateral sclerosis; lymphoid cell disorder; platelet disorder; thrombosis; periodontal disease; osteoarthritis; bone degenerative disorder; thrombosis; periodontal disease; osteoporosis; tissue repair; burn; incision; ulcer; lung; liver; severe combined immunodeficiency; SCID; autoimmune disorder; multiple sclerosis; rhematoid arthritis; allergy; asthma; thrombolysis; coagulation disorder; hereditary disorder; haemophilia; neuroprotective; antibacterial; immunosuppressive; analgesic; vulnerary; immunostimulant; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence contained in plasmid pHLZ100. Apart from the four N-terminal amino acids, it encodes the entire sequence of human pre-lysozyme C of placental origin in addition to a translational stop signal. The mature lysozyme C corresponding to the pre-lysozyme C encoded by AAN92054 has the same AA sequence as human milk lysozyme. AAN92054 differs from the nucleotide sequence of the cDNAs encoding human pre-lysozyme C isolated from human histlocytic lymphoma cell line U-937 (see FT tags a and b). However, these nucleic acid differences do not alter the amino acid
                                vaccine; vasotropic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human macrophage-expressed cDNA #17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD17740 standard; cDNA; 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 435 BP; 118 A; 79 C; 125 G; 113 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 56; ; 85pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGCACTGATTATGGGATATTTCAGATCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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/*tag= a
replace(39, "A")
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C from pichia pastoris by secretion promoter and terminator DNA
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; 1
1.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221
                             osteopathic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 435;
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CC of bio-pharmaceuticals, development of bio-sensors and transplantation.

CC The protein is used to manipulate stem cells in culture to give rise to CC neuroepithelial cells that is used to augment or replace cells damaged CC by illness, accidental damage or genetic disorders, induces the CC proliferation of neural cells and regeneration of nerve and brain tissue CC and is useful for the treatment of central and peripheral nervous system CC diseases and neuropathies, such as Alzheimer's, Parkinson's disease, CC Huntington's disease, amyotrophic lateral sclerosis and involved in CC chemotactic or chemokinetic activity, regulation of haematopolesis and CC susseful for treating lymphoid cell disorders, platelet disorders such as thrombocytopenia and osteoporosis, osteoarthritis, bone degenerative CC disorders or periodontal disease and for regeneration of bone, cartilage, CC tendon and ligament and in tissue repair, healing of burns, incisions CC and ulcers. The invention is also useful for gut protection, treatment CC severe combined immunodeficiency (SCID), bacterial or fungal infections, CC autoimmune disorders eg. multiple sclerosis, rheumatoid arthritis, autories such as asthma or other respiratory problems and is involved in thrombolysis or thrombosis is useful in treating wounds resulting CC disorders (hereditary disorders such as haemophilia) or to enhance contradian cycles of rhythms, fertility of male or female subjects, contradian cycles of rhythms, fertility of male or female subjects.
               metabolism, catabolism, anabolism, processing utilisation, storage elimination of dietary fat, lipid, protein, carbohydrate, vitamins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leukaemia and myelodysplastic syndromes. The protein exhibits activity relating to angiogenesis, cytokine, stem cell growth factor activity an activity inhibin related activities and is involved in proliferation, differentiation and survival of pluripotent and totipotent stem cells and useful tengineering damaged or diseased tissues, manufacture of him-physicals damaged or diseased tissues, manufacture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 150; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2000; 2000US-0515126
31-MAR-2000; 2000US-0540217
11-DEC-2000; 2000US-0255200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and its protein. The invention is used in gene therapy and in creating transgenic animals. Macrophage-expressed molecule is useful treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel macrophage-expressed nucleic acids and polypeptides for diagnosis and treatment of inflammatory, autoimmune, neurological, myeloid or lymphoid cell disorders, cancer and for promoting wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammatory conditions such as nephritis, Crohn's disease, ischaemia-
reperfusion injury, shock, sepsis, immune responses, cancer and myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200164839-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention relates to an isolated macrophage-expressed cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-582152/65
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68..349
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14..67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "Human mature macrophage-expressed protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Labat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ů,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein"
                                  storage or
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minerals, provides analgesic effects

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RESULT 10
AAN70943
ID AAN70
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RESULT 11
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Best Local :
                                                                                  Matches
                                                                                                        Query Match
                                                                                                                                                     A cDNA bank was constructed using total RNA isolated from the human lymphoma cell line U-937. The bank was tested by hybridising with two radio-labeled 17-mer oligonucleotides (equiv. to the AA sequences 26-31 and 63-68 of HLZ). Clones isolated were designated pHL 14-1; pHL21 and pHL 23 (contg. an approx. 500 bp insert) and pHL2 and pHL8 (contg. a 300 bp insert).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAN70943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAN70943 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 444 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed cDNA.
                                                                                                                                                                                                                                                                New hybrid plasmids contg. sequences for human lysozyme – useful e.g. as antiviral and antibacterial agent, and transformed hosts
                                                                                                                                                                                                                                                                                                                                       Sledziewski A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DE3540075-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin like activity and as an antigen in a vaccine composition to raise an immune response. The present sequence is human macrophage-
                                                                                                                                Sequence 447 BP; 122 A; 81 C; 125 G; 119 T; 0 other;
                                                                                                                                                                                                                                          Claim 5; p2; 18pp; German.
                                                                                                                                                                                                                                                                                                                  WPI; 1987-136923/20.
                                                                                                                                                                                                                                                                                                                                                                                         12-NOV-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                12-NOV-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibacterial; antiviral; bacteriolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lypozyme (HLZ).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence encoding leader or signal peptide and mature human
                                                                                                                                                                                                                                                                                                                                                               (BOEH ) BOEHRINGER INGELHEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 AAGCACTGATTATGGGATATTTCAGATCAA
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                                    192
                                               204 AAGCACTGATTATGGGATATTTCAGATCAA 233
                                                                                                                                                                                                                                                                                                      AAP70596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                 ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                        Chlebowicz-Sledziewska E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 43..432
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                                                                                                         6.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          447 BP
                                                                                  0;
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                                                                                              Score 30; Pred. No.
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Pred. No.
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                                                                                  Mismatches
                                                                                              DB 8; L
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                                    221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phagocytosis;
                                                                                                                                                                                                                                                                                                                                          Swetly P,
                                                                                                         Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 444;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which were isolated from human colon tumour and colon metastatic tumour cDNA libraries. (I) have cytostatic activity and can be used in vaccine production. (I) can be used for stimulating and/or expanding T cells specific for a tumour protein on contact with the T cells. They are also useful for inhibiting the development of cancer in a patient. (I) can be used as probes or primers for nucleic acid hybridisation, for preparing mutant species primers, or primers for use in genetic constructions. (I) can be used in the diagnosis of a colon tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated colon tumor polynucleotide differentially expressed in colon tumor or colon metastatic tumor and polypeptides encoded by them, useful for inhibiting development of cancer in patient - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JUN-2000; 2000US-210899P.
20-FEB-2001; 2001US-270216P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID 1085; 105pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; colon cancer; colon tumour antigen; cytostatic; vaccine;
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                                                                                                                                                                                                                                                                                           09-APR-1991
                                                                                                                                                                                                                                                                                                                                                     AAN70949;
                                                                                                                                                                                                                                                                                                                                                                                                            AAN70949 standard; cDNA; 490
                                                                                                             Homo sapiens
                                                                                                                                                                          Antibacterial;
                                                                                                                                                                                                                              Sequence encoding human lypozyme (HLZ) on cDNA clone HL14-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189
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30; Conserv
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                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                             antiviral;
                           Location/Qualifiers 19..454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secrist H;
                                                                                                                                                                          bacteriolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30;
Pred. No.
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1.6e-05;
                                                                                                                                                                             phagocytosis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 481;
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RESULT 13
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Best Local
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20-FEB-2001; 2001US-270216P.
                                                           WPI; 2002-114514/15.
                                                                                                            (CORI-) CORIXA CORP.
                                                                                                                                                                        08-JUN-2001; 2001WO-US18557
                                                                                                                                                                                                 20-DEC-2001.
                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                 Human; colon cancer; colon tumour antigen; cytostatic; vaccine;
                                                                                                                                                                                                                                                                                                          Human colon tumour antigen polynucleotide SEQ ID NO:1606
                                                                                                                                                                                                                                                                                                                                      08-APR-2002
                                                                                                                                                                                                                                                                                                                                                               ABL38017;
                                                                                                                                                                                                                                                                                                                                                                                   ABL38017 standard; cDNA; 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A CDNA bank was constructed using total RNA isolated from the human lymphoma cell line U-937. The bank was tested by hybridising with two radio-labeled 17-mer oligonucleotides (equiv. to the AA sequences 26-31 and 63-68 of HLZ). Clones isolated were designated pHL 14-1; pHL21 and pHL 23 (contg. an approx. 500 bp insert) and pHL2 and pHL8 (contg. a 300 bp insert).
                                                                                                                                                                                                                         WO200196388-A2
                                                                                                                                                                                                                                                                       colon tumour metastatic antigen; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 490 BP; 122 A; 100 C; 149 G; 119 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 4; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New hybrid plasmids contg. sequences for human lysozyme - ue.g. as antiviral and antibacterial agent, and transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1987-136923/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sledziewski A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New hybrid plasmids contg. sequences for human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-NOV-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-NOV-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAY-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DE3540075-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
      isolated colon tumor polynucleotide differentially expressed in tumor or colon metastatic tumor and polypeptides encoded by them I for inhibiting development of cancer in patient -
                                                                                                                                                                                                                                                                                                                                                                                                                                                211 AAGCACTGATTATGGGATATTTCAGATCAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 AAGCACTGATTATGGGATATTTCAGATCAA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP70599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BOEHRINGER INGELHEI.
                                                                                    Harlocker SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85DE-3540075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlebowicz-Sledziewska E ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85DE-3540075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.8%;
                                                                                  Secrist H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                     ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.6e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Swetly P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
This sequence represents a human nucleotide sequence which is differentially expressed in colon cancer cells compared to the expression levels in normal cells. The nucleotide sequence can be used as a source of primers and probes. The nucleotide sequence is useful for determining the phenotype of a cell by detecting the differential expression of the sequence relative to a normal cell. The probes derived from the sequence can also be used to determine the phenotype of cells in a sample. Probes and antibodies which hybridise to the nucleotide sequence can also be used to determine the phenotype of a cell. The primers are useful for detecting a mutation in a test nucleotide sequence and also for detecting cancer, preferably colon cancer. Antibodies against the protein encoded by the nucleotide sequence can also be used in a method to detect colon cancer. The diagnostic method is non-invasive and accurate for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I) which were isolated from human colon tumour and colon metastatic tumour cDNA libraries. (I) have cytostatic activity and can be used in vaccine production. (I) can be used for stimulating and/or expanding T cells specific for a tumour protein on contact with the T cells. They are also useful for inhibiting the development of cancer in a patient. (I) can be used as probes or primers for nucleic acid hybridisation, for preparing mutant species primers, or primers for use in genetic constructions. (I)
                                                                                                                                                                                                                                                        Claim 16; Page 263; 345pp; English.
                                                                                                                                                                                                                                                                                                              Novel nucleic acids and
                                                                                                                                                                                                                                                                                                                                                WPI; 2000-256641/22.
                                                                                                                                                                                                                                                                                                                                                                                                     Endege WO,
Catino TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-AUG-1998;
27-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 585 BP; 173 A; 123 C; 108 G; 179 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             can be used in the diagnosis of a colon tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID 1606; 105pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 AAGCACTGATTATGGGATATTTCAGATCAA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; detect; differential expression; human; mutation; non-invasive diagnostic method; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  colon cancer
                                                                                                                                                                                                                                                                                          nucleic acids and proteins for identifying therapeutic agents for treating and diagnosing cancer, especially colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30;
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                                                                                                                                                                                                                                                                                                                                                                                          Steinmann KE, As...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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99US-0117393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          differentially expressed nucleotide sequence #344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.8%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   JH, Burgess CC, Carroll E;
Lewis ME, Molino GA, Mona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 24;
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                                                                                                                                                                                                                                                                                                                                                                                                     Monahan JE;
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colon cancer at an early stage.

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                                                                                                                                                                                                                                                                CC expressed in cancer tissues. ABB/893 to ABB/9004 represent proteins and central proteins are encoded by the AB060776 to AB060787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide cc encoded by (I) is useful for detecting cancer in a patient sample, and cc for detecting the presence or absence of a polynucleotide encoded by a cucleic acid which hybridises to (I) in a cell. A probe/primer derived cc from (I) can be used for determining the presence of a nucleic acid which hybridises to (I) in serious the phenotype of cells in a sample cc of cells from a patient. (I) is useful for determining the presence of sample cc of cells from a patient. (I) is useful for determining the presence of cc olon cancer in a cell or tissue type, for determining the presence or cc state of other type of cancer, in antisense therapy, to generate cc macroarrays on a solid surface, to identify a chromosome on which the ccorresponding gene resides, and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise cc antibodies, and to screen for peptide analogues and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.8%; Score 30; DB 21; Best Local Similarity 100.0%; Pred. No. 1.6e-05 Matches 30; Conservative 0; Mismatches (
                                                                                                     Query Match
Best Local Similarity
                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             puryess C, Astle JH, Carroll E, Thiaglingam A, Lewis ME;
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                                                                                                                                                                                                          Sequence 706 BP; 196 A; 156 C; 134 G; 206 T; 14 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 1; 796pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200229086-A2.
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204 AAGCACTGATTATGGGATATTTCAGATCAA 233
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                                                                        30;
                                                                6.8%; Score 30; DB 24; ilarity 100.0%; Pred. No. 1.6e-05 Conservative 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Catino TJ,
                                                                1.6e-05;
hes 0;
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                                                                                                                                 Length 706;
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Db 516 AAGCACTGATTATGGGATATTTCAGATCAA 487

Search completed: July 5, 2003, 06:20:13 Job time : 182 secs

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ALIGNMENTS

	COMMENT	REFERENCE AUTHORS TITLE	ORGANISM	ACCESSION VERSION KEYWORDS	RESULT 1 BG937925 LOCUS DEFINITION
Tel: 780 492 0169 Fax: 780 492 0169 Fax: 780 492 4265 Email: smooredains.ualberta.ca The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA) in main database at high score of 898.0 and E-value of 0.0 PCR PRimers FORWARD: M13 Forward BACKWARD: M13 Reverse	Contact: Dr. Stephen Moore Contact: Dr. Stephen Moore Beef Genomics Laboratory Dept of AFNS, University of Alberta 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada	1 (bases 1 to 453) Moore,S.S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G. cDNA's from bovine abomasum tissue Thoublished (2001)	BOS taurus BOS taurus Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.	lence. 17925 17925.1	BG937925 453 bp mRNA linear EST 11-JUN-2001 1Abo09H04 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA

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KEYWORDS
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Mammalia; E
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 Contact: Dr.
              Unpublished
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                           cDNA's from
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                                                                             Eutheria;
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/sex="Two males and one female mixed"
/tissue_Type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
/dev_stage="Young adult"
/leb_host="XLI-BlueMRF'-strain"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
I; Site_2: Xho I"
87 c 121 g 116 t
                                                                                        Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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          bovine abomasum tissue (2001)
                                       Hansen, C., Li, C.,
Stephen Moore
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                                   Fu, A.,
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                              1Abo16E03 Bovine Abomasum
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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Seq primer: T3 primer
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The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA) in main database at high score of 916.0 and E-value of 0.0
                                                                                                                                                                                                                               CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT 420
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I; Site_2: Xho I"
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA's from bovine abomasum tissue
Unpublished (2001)
Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae; B
1 (bases 1 to 463)
Moore, S.S., Hansen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Crahiata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: T3 primer High quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORWARD: M13 Forward BACKWARD: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence best matches gb:BOVLZYM7A (Bos) in main database at high score of 918.0 an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                             TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                                                                                                                                                                                                                                                                                                           GTCAGCCTGGCAAACTGGTTGTGTTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT 180
                                                                                                                                                                                                                                                                                                                                                                             TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA
                                 CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT
                                                                                                                                                                       TGGTGGTGTAATGATGGCAAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="XL1-BlueMRF'-strain"
/note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
/cell_type="Epithelial"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Bos taurus"
/db_xref="taxon:9913"
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91 c 119 g
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Pred. No. 1.5e-223;
); Mismatches 0;
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REFERENCE
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BG938413
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254
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                                                                                                                                                           121 GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT 180
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                                                                                                                                                                                                                                 61 TTTGAGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120
                                                                                                                                                                                                                                                                                   14 ATGAAGGCTCTCGTTATTCTGGGGGTTTCTCTTTCTGTCGCTGTCCAAGGCAAGGTC
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BG938413
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1Abo07G10
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 464)
Moore, S.S., Hansen, C., Li, C., Fu, A.,
cDNA's from bowline abomasum tissue
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: smoore@afns.ualberta.ca
The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA)in main database at high score of 920.0 and E-value of 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG938413.1
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                                                                                                                                                                                                                                                                                                  ATGAAGGCTCTCGTTATTCTGGGGTTTCTTCTTTCTTCTGTCGCTGTCCAAGGCAAGGTC 60
            TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC 300
                                                                                      ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 240
                                                                                                                                        GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAAACACAAAAGCT 193
                                                                                                                                                                                                                TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 133
TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
                                                                    ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                              132
                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="XL1-BlueMRF'-strain"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
I; Site_2: Xho I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Bovine Abomasum cDNA Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="Young adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                                                                                            121 g
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Pred. No. 1.5e-223;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                        Length 464;
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BG938112
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AUTHORS
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                                                                                                                                           Local
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                                61
                                                               17
                                                          BACKWARD: M13 Reverse
Seq primer: 13 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FORWARD: M13 Forward BACKWARD: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: smoore@afns.ualberta.ca
The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme) in main database at high score of 930.0 and E-value of 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dept of AFNS, University of Alberta 410 Agri/For, Dept of AFNS, U of A,
                                                                                                                                                                                                                                                                                                                                                                                                             POLYA-No.
                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moore, S.S., Hansen, C., Li, C., Fu, A CDNA's from bovine abomasum tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG938112 469 bp mRNA linear lAbol1D12 Bovine Abomasum cDNA Library Bos taurus
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                                                                                                                                           Similarity
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
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                                                                                                                                                                                                          133
                                                                                                                             Conservative
                                                                                                                                                                                                    /tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
/dev_stage="Young adult"
/lab_host="XL1-BlueMRF'-strain"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
I; Site_2: Xho I"
; Site_2: 123 g 121 t
                                                                                                                                                                                                                                                                                                                           /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="Bovine Abomasum cDNA Library"
                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   /sex="Two males and one female mixed"
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                                                                                                                                         100.0%; Score 444; DB 13; 100.0%; Pred. No. 1.5e-223;
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                                                                                                                            0;
                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Edmonton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Meng, Y.
                                                                                                                            0;
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                                                                                                                         Indels
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CDNA 5', mRNA
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                         Seq primer: T3 primer High quality sequence
                                                                                                                                                                                                                                                                                          BACKWARD: M13 Reverse
                                                                                                                                                                                                                                                                                                                                             The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA)in main database at high score of 944.0 and E-value of 0.0
                                                                                                                                                                                                                                                                                                                                                                                              Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moore, S.S., Hansen, C., Li, C., Fu, A., CDNA's from bovine abomasum tissue
                                                                                                                                                                                                                                           POLYA-No.
                                                                                                                                                                                                                                                                                                                                                                               Email: smoore@afns.ualberta.ca
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Bovine Abomasum cDNA
            /note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
94 c 122 g 125 t
                                                                                                /clone_lib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
/tlssue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
                                                               /dev_stage="Young adult"
/lab_host="XL1-BlueMRF'-strain"
                                                                                                                                                                      /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                       Location/Qualifiers
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High quality sequence stop: 476
                                                                                                                                                   The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme) in main database at high score of 944.0 and E-value of 0.0
                                                                                                                                                                                              Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                      Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
                                                                                                                                                                                                                                                               Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                           Unpublished (2001)
                                                                                                                                                                                                                                                                                          cDNA's from bovine abomasum tissue
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                                                                        POLYA-No
                                                                                                            BACKWARD: M13 Reverse
                                                                                                                            FORWARD: M13 Forward
                                                                                                                                          PCR PRimers
                                                                                                                                                                              Email: smoore@afns.ualberta.ca
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 /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="Bovine Abomasum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78
The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA) in main database at high score of 948.0 and E-value of 0.0
                                                                                                                                                                                                                                      COW
                                                                                                                                                                                                                                                                           sequence.
BG937601
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438 TACGTTGAGGGTTGCACCCTGTAA
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               Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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                                                                                                                        Contact: Dr. Stephen Moore
                                                                                                                                         CDNA's from bovine abomasum Unpublished (2001)
                                                                                                                                                                                  Moore, S.S., Hansen, C., Li, C., Fu, A.,
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                                                                                                 BG937601.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                              1Abo03H1 Bovine
Email: smoore@afns.ualberta.ca
                                                                                                                                                                                                                              Bovidae; Bovinae;
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                                                                                                                                                                                                      (bases 1 to 478)
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/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
I; Site_2: Xho I"
1 93 c 123 q 125 +
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/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
/dev_stage="Young adult"
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Pred. No. 1.5e-223;
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VA 5', mRNA
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REFERENCE
AUTHORS
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                                                                                                              KEYWORDS
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                                                                                                                                             ACCESSION
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                                  Bovidae; Bovinae; Bos.
                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                               Bos taurus
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                                                                                                                             BG937832.1
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Seq primer: T3 primer
Moore, S.S., Hansen, C., Li, C.,
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                (bases 1 to 481)
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/lab_host="XL1-BlueMRF'-strain"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
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95 c 123 g 125 t
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/db_xref="taxon:9913"
/clone_lib="Bovine Abomasum cDNA Library"
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/tlssue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
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Pred. No. 1.5e-223;
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
BG937936 4
1Abo08E01 Bovine Abomasum
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The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA)in main database at high score of 954.0 and E-value of 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA's from bovine abomasum
Unpublished (2001)
Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop:
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/note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
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/cell_type="Epithelial"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Two males and one female mixed"
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Pred. No. 1.5e-223;
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                                                                                                                                     241 TGGTGGTGTAATGATGGCAAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
                                                                                                                                                                                         192
                                                                                                                                                                                                                                                                           121 GTCAGCCTGGCAAACTGGTTGTGTTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT
                   361
                                                                                   301
                                                                                                                                                                                                                         181 ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
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BG937936.1
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Contact: Dr. Stephen Moore
Beef Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moore,S.S., Hansen,C., Li,C., Fu,A., cDNA's from bovine abomasum tissue
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Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: T3 primer High quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: smoore@afns.ualberta.ca |
The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme ')
) in main database at high score of 955.0 and E-value of 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovidae; Bovinae;
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Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                   CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT
                                                   GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                                                                     GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                                                                                                                                                                       ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                                                                                     {	t TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC}
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Conservative
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/note="Organ: Abomasum; Vector: Uni-2ZAPXR;
I; Site_2: Xho_I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial" |
/dev_stage="Young adult" |
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/db_xref="taxon:9913" |
/clone_lib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
/sex="Two males and one female mixed"
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                                          181 ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 240
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410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moore, S.S., Hansen, C., Li, C., Fu, A., cDNA's from bovine abomasum tissue
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1Abo09C06 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA
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The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA) in main database at high score of 959.0 and E-value of 0.0
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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I; Site_2: Xho I"
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/lab_host="XL1-BlueMRF'-strain"
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/sex="Two males and one female mixed"
/tissue_type="castrointestinal tissue (GIT)"
/cell_type="Epithelial"
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/db_xref="taxon:9913"
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1Abo13G04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moore,S.S., Hansen,C., L1,C., cDNA's from bovine abomasum t. Unpublished (2001)
Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: T3 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA) __in main database at high score of 961.0 and E-value of 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: smoore@afns.ualberta.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 780 492 4265
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                  ATGAAGGCTCTCGTTATTCTGGGGTTTCTCTTCTTTCTGTCGCTGTCCAAGGCAAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGCCTGTCATGTATCCTGCAGC
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                                                                                                                                                                                  137
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: 485
                                                                                                                                                                                                               /lab_host="XL1-BlueMRF'-strain"
/note="Organ: Abomasum; Vector:
                                                                                                                                                                                                                                                                  /clone_lib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                    /dev_stage="Young adult"
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Pred. No. 1.6e-223;
Mismatches 0;
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BG937882
                                                                                                                                                                                                                                                                                                                                                                    Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA's from bovine abomasum Unpublished (2001)
Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                           FORWARD: M13 Forward BACKWARD: M13 Reverse Seq primer: T3 primer
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Moore, S.S., Hansen,
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                                                                                                                                                                                                                                                                                                                                   The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme
                                                                                                                                                                                                                                                                                                                                                 Email: smoore@afns.ualberta.ca
                                                                                                                                                                                                                                                                                                                    ij
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                                                                                                                                                                                                                                                                                                                main database at high score of
                                                                                                                                                                                                                            quality sequence stop: 486
/note="Organ: Abomasum; Vector: Uni-22APXR; Site_1: Ecor
I; Site_2: Xho I"
                                                                                  /sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
                                                                                                                 /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="Bovine Abomasum cDNA Library"
                                 /dev_stage="Young adult"
/lab_host="XL1-BlueMRF'-strain"
                                                                   /cell_type="Epithelial"
                                                                                                                                                                                         Location/Qualifiers
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EST 11-JUN-2001 CDNA 5', mRNA

T6G 2P5,

7A mRNA

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Gaps

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BG938101
                                                                                                                                                                           Contact: Dr Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
                                                                     PCR PRimers
FORWARD: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                          EST
                 POLYA-No.
                                           Seq primer: T3 primer
                                                          BACKWARD: M13 Reverse
                                                                                                    The sequence best matches gb:BOVLZYM7A (Bos taurus lys) in main database at high score of 963.0 and E-value
                                                                                                                                   Email: smoore@afns.ualberta.ca
                                                                                                                                                                                                                                     Unpublished (2001)
                                                                                                                                                                                                                                                      Moore, S.S., Hansen, C., Li, C., Fu, A., cDNA's from bovine abomasum tissue
                                                                                                                                                                                                                                                                                                 Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                             Eukaryota;
                                                                                                                                                                                                                                                                                                                                              Bos taurus
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780 492 4265
                              quality sequence stop: 486
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Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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TITLE
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CDNA's from bovine abomasum tissue
Unpublished (2001)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta 410 Agri/For, Dept of AFNS, U of A, Tel: 780 492 0169
                                                                                                                                                                                            COW.
                                                                                                                                                                                                                                                                  BG938250 487 bp mRNA linear EST 11-JUN-2001 1Abol4E01 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA
                                                                                                                                   Bovidae; Bovinae;
                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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/db_xref="taxon:9913"
/clone_lib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
/tissue_type="castrointestinal tissue (GIT)"
/cell_type="Tepithelial"
/dev_stage="Young adult"
/dev_stage="Young adult"
/lab_host="Xil-BlueMRE'-strain"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Sit
I; Site_2: Xho I"
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BACKWARD: M13 Reverse
Seq primer: T3 primer
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The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA)
in main database at high score of 965.0 and E-value of 0.0
                                                                                                                                                                                                                                            ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 240
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                                                             TACGTTGAGGGTTGCACCCTGTAA 460
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/lab_host="Xil-BlueMRF'.strain"
/note="Organ: Abomasum; Vector:
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97 c 124 g 129 t
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/sex="Two males and one female mixed"
/tlssue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
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/db_xref="taxon:9913"
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Maximum DB seq length: 2000000000
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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US-08-621-100-11
US-08-071-601-11
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US-08-071-601-11
US-08-08-726-883-7
US-08-726-883-8
US-08-726-883-12
US-08-726-883-12
US-08-726-883-12
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US-09-123-912-32	US-09-040-984-32	US-09-328-111-342	US-09-134-001C-2480	US-08-133-711-40	US-09-134-001C-1740	US-09-397-787-296	US-09-134-001C-2435	US-08-865-960-16	US-09-151-189-5	US-09-453-702B-50	US-08-472-809B-7	US-08-472-809B-8	US-08-437-362-1	US-08-220-401-1	US-08-687-956A-22	PCT-US92-08756A-3	US-08-309-512-3
Sequence 32, Appl	Sequence 32, Appl	Sequence 342, App	Sequence 2480, Ap	Sequence 40, Appl	Sequence 1740, Ap	Sequence 296, App	Sequence 2435, Ap	Sequence 16, Appl	Sequence 5, Appli	Sequence 50, Appl		Sequence 8, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 22, Appl	Sequence 3, Appli	Sequence 3, Appli

ALIGNMENTS

RESULT 1 US-07-798-223A-1

Sequence 1, Application US/07798223A Patent No. 5422108 GENERAL INFORMATION:

APPLICANT: Mirkov, T. Erik
APPLICANT: Fitzmaurice, Leona Claire
TITLE OF INVENTION: Protection of Plants Against Pathogens
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

ADDRESSEE:

E: Fitch, Even, Tabin & Flannery
135 South LaSalle Street, Suite 900

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US-07-798-223A-1
  Query Match
Best Local Sim
Matches 439;
                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WOOTDERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/798,223A
FILING DATE: 19911125
CLASSIFICATION DATA:
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/762,679
FILING DATE: 19-SEP-1991
AFTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 51984
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION STEPPANION: 0619)552-1311
TELECHMUNICATION POBERT: 50.51
                                                                                                                                                                                                                                                                                               TELEFAX: (619)552-0095
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                   FEATURE:
                                                                                                                                                                           MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 964 base pairs
                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: unk
                                                                                                                                                                                                                TYPE: NUCLEIC ACID STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 135 Sc
CITY: Chicago
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                          Similarity
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98.9%; Score 439; DB 1; L4
100.0%; Pred. No. 1.5e-226;
tive 0; Mismatches 0;
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                                           DB 1; Length 964;
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Conservative

Indels

0;

Gaps

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GENERAL INFORMATION:

APPLICANT: ENDEGE, WILSON O., ET AL.

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: PRODUCTS: II

FILE REFERENCE: CCDNA-260XX

CURRENT APPLICATION NUMBER: US/09/385,982

CURRENT FILING DATE: 1999-08-30

EARLIER APPLICATION NUMBER: 09/328,111

EARLIER FILING DATE: 1999-06-08

EARLIER FILING DATE: 1999-01-27

EARLIER APPLICATION NUMBER: 60/198,639

EARLIER APPLICATION NUMBER: 60/098,639
RESULT 3
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                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 344 LENGTH: 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 344, Application US/09385982
Patent No. 6262334
                                                                                                                                       Query Match
                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                          EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: (1)...(657) OTHER INFORMATION: n -
                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                         Local Similarity
                                                           204 AAGCACTGATTATGGGATATTTCAGATCAA 233
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                                           AAGCACTGATTATGGGATATTTCAGATCAA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAGCAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAGGGTTGCACCCTGTAA 462
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                                                                                                          Conservative
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (608) 255-2182
TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                              NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2044 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: F.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BLECK, GREGORY T. APPLICANT: BREMEL, ROBERT D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                        LENGTH: 2044 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
2036 CAGCCTGGGTGGCATGGAA 2018
                          371 CAGCCTGGGTGGCATGGAA 389
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                                                                      Similarity
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                                                         Conservative
                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                              RNA polymerase binding region 1961..1978
                                                                                                                                                                                                                        inherited control region for a-lactalbumin 1966
                                                                                                                                                                             putative steroid response element 1433..1446
                                                                                                                                                                                                                                                                    signal peptide coding region 1943..2043
                                                                                                                                                                                                                                                                                                                                                                                                                                  (608) 255-2022
508) 255-2182
                                                                                                                                                                                                                                                                                                            DNA (genomic)
                                                                    100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/07/744,765
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                                                        0;
                                                                    Score 19;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3262-1
                                                         Mismatches
                                                                      DB 1;
0.91;
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1100
                                                        0;
                                                                                    Length 2044;
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                                                      0;
                                                      Gaps
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US-08-621-100-3/c

0;

Sequence 3, Application US/08621100 Patent No. 5850000

GENERAL INFORMATION:

APPLICANT:

BLECK, O

GREGORY T.

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US-08-071-601-15; Sequence 15, Application US/08071601; Patent No. 5530177;
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                                                                                                                                                           RESULT 5
                                                                                                                                                                                                                                                                       Matches
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                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (608) 255-2182
TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2044 base pairs
           APPLICANT: BLECK, GREGORY T.
APPLICANT: BREMEL, ROBERT D.
TITLE OF INVENTION: DNA SEQUENCE ENCOD
TITLE OF INVENTION: ALPHA-LACTALBUMIN
NUMBER OF SEQUENCES: 20
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/744,765
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REGISTRATION NUMBER:
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                                                                                                                                                                                                         2036 CAGCCTGGGTGGCATGGAA 2018
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100.0%; Pr
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                                             DNA SEQUENCE ENCODING
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                              METHODS OF USE
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL
STREET: 100 E. WISCONSIN AVE., SUITE 1100
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APPLICATION NUMBER: 1
             CLASSIFICATION: 800 PRIOR APPLICATION NUMBER:
                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 22-MAR-19
                                                                                                                                                                     ZIP: 53202-4178
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BLECK, GREGORY T. APPLICANT: BREMEL, ROBERT D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: LUC
CTTY: MILWAUKEE
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TELEX: 26832 ANDSTARK
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                                                                                                                                                                                        COUNTRY: USA
ZIP: 53202-4178
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FILING DATE:
                                                                                                            SOFTWARE:
                                                                                                                                                           MEDIUM TYPE: Floppy disk
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                                                                                                            PatentIn Release #1.0, Version #1.25
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                                                              22-MAR-1996
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.00.0%; Pred. No.
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US-08-851-190-4
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                                                                                                           INFORMATION FOR SEQ ID NO:
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TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO:
                                                                                                                                                      REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                           SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskette
TOPOLOGY: line
IMMEDIATE SOURCE
LIBRARY: TONSI
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for I
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CORRESPONDENCE ADDRESS:
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MOLECULE TYPE:
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LENGTH: 20 base pairs
TYPE: nucleic acid
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                                            STRANDEDNESS:
                                                                                                                                       TELEFAX: 415-845-4166
                                                                                                                                                                                              NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
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REGISTRATION NUMBER:
                                                                            ENGTH:
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                                                            nucleic acid
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3174 Porter Drive
 TONSNOT 01
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100.0%; Pred. No.
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RESULT 9
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; ORGANISM: Oryza sativa
US-09-291-922-21
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APPLICANT: Allen, Steve
APPLICANT: Hitz, Bill
APPLICANT: Kinney, Tony
APPLICANT: Tingey, Scott
TITLE OF INVENTION: Plant Sugar Transport Proteins
FILE REFERENCE: BB-1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Microsoft Office 97
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/08071601 Patent No. 5530177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/291,922
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: 60/083,044
EARLIER FILING DATE: April 24, 1998
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                      CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2017
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BLECK, GREGORY T.
APPLICANT: BREMEL, ROBERT D.
TITLE OF INVENTION: DAY SEQUE
TITLE OF INVENTION: ALPHA-LAC
                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 53202-4178
                                     APPLICATION NUMBER:
                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                         CITY: MILWAUKEE
STATE: WI
                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1413 CTGTCGCTGTCCAAGGC 1429
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                                                                                                                                                                                                                                                                                                     E: ANDRUS, SCEALES, STARKE & SAWALL 100 E. WISCONSIN AVE., SUITE 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.8%; Score 17; DB 100.0%; Pred. No. 10;
                                     US/07/744,765
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                                                                                                        US/08/071,601
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US-08-621-100-11
                              TELEFAX: (608) 255-2182
TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
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                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: SAIR, Charles S
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: F. 3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 255-28022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: F. TELECOMMUNICATION INFORMATION: TELEPHONE: (608) 255-2022
                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 53202-4178
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: BREMEL, ROBERT D.
TITLE OF INVENTION: DNA SEQUITITLE OF INVENTION: ALPHA-LAG
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 800 PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 43 base pairs TYPE: nucleic acid STRANDEDNESS: single
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TELEX: 26832 ANDSTARK
                                                                                                                                                                                                                                                                         FILING DATE:
APPLICATION NUMBER: US/07/744,765
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08 FILING DATE: 22-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sara, Charles S
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
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                                                                                                                                                      2: (608) 255-2022
(608) 255-2182
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                DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA SEQUENCE ENCODING BOVINE ALPHA-LACTALBUMIN AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                              US/08/621,100
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US-08-419-078-7
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US-08-726-883-7
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                                                                                                            Sequence 7, Application US/08726883 Patent No. 5676946
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Best Local :
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                                                                                                                                                                                                                                                                            Matches
                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-855-0572
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDI
IMMEDIATE SOURCE:
LIBRARY: Human I
CLONE: 067172
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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MEDIUM TYPE: Floppy
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ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3330 HILLVIEW AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HAWKINS, PHILLIP R.
APPLICANT: SEILHAMER, JEFFREY J.
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
NUMBER OF SEQUENCES: 13
                            APPLICANT: HAWKINS, PHILLIP R.
APPLICANT: SETLHAMER, JEFFREY J.
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: PALO ALTO
                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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100.0%; Pi
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.00.0%; Pred. No.
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                                                                                                                                                                                                                                                                            0;
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STREET: 33...
CTTY: PALO ALTO

3330 HILLVIEW AVENUE

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RESULT 13
US-08-419-078-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08419078 Patent No. 5587306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: HAWKINS, PHILLIP R.

APPLICANT: SEILHAMER, JEFFREY J.

TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3330 HILLVIEW AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-855-0572
INFORMATION FOR SEQ ID NO:
FILING LALL 435
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
NAME: LUTHER, BARBARA J.
                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,078
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LIBRARY: Human Fetal Endothelial - Stressed
CLONE: 067172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 180 base pairs
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COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
**TATTATATA WINDER: 0709/776 083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/419,078
FILING DATE: 10-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 415-855-0555
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                                                                                                                                                                                                                                                                    STREET: 3330 HIJ
CITY: PALO ALTO
                                                                                                                                                                                                                      COUNTRY: US
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/726,883 FILING DATE: 04-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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Pred. No.
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US-08-726-883-8
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08726883 Patent No. 5676946
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                                                                                                                                                                                             TELEFAX: 415-855-0572
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                             IMMEDIATE SOURCE:
LIBRARY: Human
CLONE: 067990
                                                                                               TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 191 base pairs
                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         FILING DATE: 10-APR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/419,078
FILING DATE: 10-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
LIBRARY: Human Fetal Endothelial - Stressed
CLONE: 067990
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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ADDRESSEE: INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HAWKINS, PHILLIP R.
APPLICANT: SEILHAMER, JEFFREY J.
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
NUMBER OF SEQUENCES: 13
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CLASSIFICATION:
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                                                            Human Fetal Endothelial - Stressed
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100.0%; Pred. No.
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Score 16;
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DB 1;
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Length 191;
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CIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,078

FILING DATE:
APPLICATION NUMBER: US/08/419,078

FILING DATE:
APTORNEY/AGENT INFORMATION:
APETERNICATION NUMBER: 33954

REGISTRATION INFORMATION:
TELEPHONE: 415-855-0555

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0572
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
LIBRARY: Inflamed Adenoid
LIBRARY: Inflamed Adenoid
LIBRARY: 159363

US-08-419-078-12
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Search completed: July 5, 2003, 07:05:49 Job time: 43 secs
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US-08-419-078-12
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APPLICANT: SEILHAMER, JEFFREY J.
TITLE OF INVENTION: PHOSHOLIPASE C HOMOLOG
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC;
STREET: 3330 HILLVIEW AVENUE
CITY: PALO ALTO
STATE: CA
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ZIP: 94304
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16; Conservative 0; Mismatches
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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equence 34, Apple equence 117, App Sequence 117, App Sequence 5474, Apple equence 558, Apple equence 590, Apple Sequence 290, Appli Sequence 3, Appli Sequence 3, Appli equence 21, Apple equence 21, Appli equence 4, Appli equence 4, Appli equence 4, Appli equence 5, Appli	App
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APPLICANT: POGUE, GREGORY P.
APPLICANT: VELICHKO, SHARLENE
APPLICANT: VELICHKO, SHARLENE
TITLE OF INVENTION: PRODUCTION OF BOVINE LYSOZYME BY PLANT VIRAL VECTORS
                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 444; DB 10; Best Local Similarity 100.0%; Pred. No. 1.2e-232; Matches 444; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1
LENGTH: 444
TYPE: DNA
ORGANISM: Bovine sp.
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Patent No. US20020104126A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/978,199
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 60/240,967
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.1
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                                      181 ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 240
                                                                                                                    61 TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAACTTGGACTGGACGGCTATAAGGGA 120
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US-09-978-199-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/978,199
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 60/240,967
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: POGUE, GREGORY P.
APPLICANT: VELICHKO, SHARLENE
TITLE OF INVENTION: PRODUCTION OF BOVINE LYSOZYME BY PLANT VIRAL VECTORS
FILE REFERENCE: 42202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
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                             CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT 420
                                                                                               GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                                                                                                GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG 360
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RESULT 4
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PRIOR FILING DATE: 2000-03-01
PRIOR PRIOR APPLICATION NUMBER: 60/200,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR FILING DATE: 2000-05-02
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                                                                 Sequence 8055, Application US/10040862 Publication No. US20030078396A1 GENERAL INFORMATION:
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 8055
LENGTH: 367
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APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A. APPLICANT: Mannion, Jane
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APPLICANT: Algate, Paul A.
APPLICANT: Manion, Jane
APPLICANT: MANION, COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
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PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING DATE: 2000-08-04
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NAME/KEY: unsure
LOCATION: (361)
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NAME/KEY: unsure
LOCATION: (331)
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30; Conserv
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LENGTH: 367
                                                                                                                                                                                            Sequence 3129, Application US/10066543 Publication No. US20030087818A1
                                                                                                                                                                             GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                     APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
                                                                                                                                        APPLICANT: Jiang, Yuqiu APPLICANT: Pyle, Ruth A.
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NUMBER OF SEQ ID NOS: 10467
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CURRENT FILING DATE: 2001-11-06
                                                      APPLICANT:
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PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR FILING DATE: 2000-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
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                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (361)
OTHER INFORMATION: n-A,T,C or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: unsure LOCATION: (331)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/223,378
                                                                                                                                                                             INFORMATION:
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              Fanger, Gary R. Smith, Carole L.
                                                Secrist, Heather
Carter, Darrick
                                                                                       Lodes, Michael J.
                                                                                                      Xu, Jiangchun
Indirias, Carol Yoseph
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Durham, Margarita
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100.0%; Pred. No
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LENGTH: 446
TYPE: DNA
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LENGTH: 478
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                SEQ ID NO 1085
LENGTH: 478
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APPLICANT: Stolk, John A.
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Secrist, Heather
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Sequence 1085, Application US/09878178
Patent No. US20020177552A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527
CURRENT APPLICATION NUMBER: US/09/878,178
CURRENT FILING DATE: 2001-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1085, Application US/10046935 Patent No. US20020156011A1
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TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.563
CURRENT FILING NUMBER: US/10/066,543
CURRENT FILING DAVE: 2002-01-31
NUMBER OF SEQ ID NOS: 3417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.527C1
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NUMBER OF SEQ ID NOS: 2237
SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
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00.0%; Pred. No.
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hes 0;
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US-10-102-524-791
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER
FILE REFERENCE: 210121.572
CURRENT APPLICATION NUMBER: US/10/102,524
CURRENT FILING DATE: 2002-03-19
NUMBER OF SEQ ID NOS: 1863
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 791
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Gaiger, Alexande
APPLICANT: Gordon, Brian
APPLICANT: Harlocker, Susar
Query Match
Best Local Similarity
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Publication No. US20030109434A1
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LENGTH: 478
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Best Local Similarity
Matches 30; Conserv
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APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527C2
CURRENT FILING DATE: 2002-05-14
NUMBER: 05-10 NOS: 2241
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APPLICANT: Harlocker, APPLICANT: Secrist, He
                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: 447, 456, 466
OTHER INFORMATION: n = 1
                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                             LENGTH: 522
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Gordon, Brian
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6.8%;
100.0%;
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Pred. No.
Score 30;
Pred. No.
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DB 9; L
3.6e-06;
               Length 522;
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RESULT 12
US-10-146-502-1606/c
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1606
; LENGTH: 582
; TYPE: DNA
; ORGANIZM: Homo sapiens
US-10-046-935-1606
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US-09-878-178-1606/c
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                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/878,178
CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 2237
SOFTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 1606
LENGTH: 582
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                                                                                                                                              Matches
                                                                                                                                                                             Query Match
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                                                                                                                                                                Best
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APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jiang, Yuqiu
APPLICANT: Harlocker, Susan
APPLICANT: Secrist, Heather
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.527C1
CURRENT APPLICATION NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Aijun APPLICANT: Stolk, John A.
                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                       511 AAGCACTGATTATGGGATATTTCAGATCAA 482
                                                                                                         204 AAGCACTGATTATGGGATATTTCAGATCAA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              511 AAGCACTGATTATGGGATATTTCAGATCAA 482
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                                                                                                                                            30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30;
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                                                                                                                                                            Similarity
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                                                                                                                                            Conservative
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                                                                                                                                     , 100.0%; Pr
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                                                                                                                                                           6.8%; Score 30; DB 9; L
100.0%; Pred. No. 3.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30; DB 9; I pred. No. 3.7e-06;
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                                                                                                                                         Mismatches
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                                                                                                                                                                           Length 582;
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                                                                                                                                           Indels
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Sequence 1606, Application US/10146502; Publication No. US20030069180A1

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CURRENT APPLICATION NUMBER: US/10/146,502
CURRENT FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2241
SOFTWARE: FBSATSEQ for Windows Version 4.0
SEQ ID NO 1606
LENGTH: 582
TYPE: DNA
ORGANISM: Homo sapiens
US-10-146-502-1606
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                                                                                                            RESULT 14
US-09-796-692-8226
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APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Persing, David H.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yuqiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2544
LENGTH: 606
TYPE: DNA
                                                     Sequence 8226, Application US/09796692 Publication No. US20020198362A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/060,036 CURRENT FILING DATE: 2002-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.527C2
                                 APPLICANT: Gaiger, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF PANCHEATIC CANCER
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                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: n = A, T, C or G
                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: 603
                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 6.8%; Score 30; Local Similarity 100.0%; Pred: No. es 30; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 AAGCACTGATTATGGGATATTTCAGATCAA 233
                                                                                                                                                                                     511 AAGCACTGATTATGGGATATTTCAGATCAA 482
                                                                                                                                                                                                        204 AAGCACTGATTATGGGATATTTCAGATCAA 233
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Secrist, Heather
Mannion, Jane
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                   Algate, Paul A.
                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                 6.8%; Score 30; 100.0%; Pred. No.
                                                                                                                                                                                                                                                               0;
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hes 0;
                                                                                                                                                                                                                                                                                                     DB 9;
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                                                                                                                                                                                                                                                                                                                                               Publication No. US20 GENERAL INFORMATION:
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NAME/KEY: unsure
LOCATION: (603)

OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (615)
                                                                                                                                                                                                                                                                                                                                                                     Sequence 8226, Application US/10040862 Publication No. US20030078396A1
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LENGTH: 636
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            CURRENT FILING DATE: 2001-11-06

PRIOR APPLICATION NUMBER: US/10/040,862

CURRENT FILING DATE: 2001-11-06

PRIOR PELICATION NUMBER: US 60/186,126

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: US 60/190,479

PRIOR FILING DATE: 2000-03-17
                                                                                                                                                                                                                                              APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
                                                                                                                                                       TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and The: TITLE OF INVENTION: Hematological Malignancies FILE REFERENCE: 014058-013520US
                                                                                                                                                                                                                           APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-0
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PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THE
PRIOR APPLICATION NUMBER: US 60/200,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,378
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PRIOR FILING DATE: 2000-04-27
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PRIOR FILING DATE: 2000-03-17
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PRIOR APPLICATION NUMBER: 60/186,126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/222,903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/218,950 FILING DATE: 2000-07-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 AAGCACTGATTATGGGATATTTCAGATCAA 233
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100.0%; Pred. No. 3.7e-(
tive 0; Mismatches
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...URE FILING DATE: 2000-04-27

PRIOR PELICATION UNMBER: US 60/200,799

PRIOR APPLICATION UNMBER: US 60/200,799

PRIOR PRIOR APPLICATION UNMBER: US 60/200,999

PRIOR PRIOR PELICATION UNMBER: US 60/200,099

PRIOR PRIOR PELICATION UNMBER: US 60/200,099

PRIOR PRIOR PELICATION UNMBER: US 60/200,099

PRIOR PRIOR APPLICATION UNMBER: US 60/200,094

PRIOR APPLICATION UNMBER: US 60/200,084

PRIOR APPLICATION UNMBER: US 60/200,204

PRIOR APPLICATION UNMBER: US 60/202,084

PRIOR APPLICATION UNMBER: US 60/202,084

PRIOR PELICATION UNMBER: US 60/202,093

PRIOR PELICATION UNMBER: US 60/202,3416

PRIOR PELICATION UNMBER: US 60/223,378

PERIOR P
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